

SEQUENCE LISTING



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 The Government of the United States of America
 as represented by the Secretary of the
 Department of Health and Human Services

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JAN 19 2001

TECH CENTER 1600/2900

<120> T2R, a Novel Family of Taste Receptors

<130> 02307E-098010US

<140> US 09/510,332
 <141> 2000-02-22

<150> US 09/393,634
 <151> 1999-09-10

<160> 172

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JAN 23 2001

TECH CENTER 1600/2900

<170> PatentIn Ver. 2.1

<210> 1

<211> 299

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R01 (hGR01)

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Ile	Asp	Leu	Ile	Lys	His	Arg	Lys	Met	Ala	Pro	Leu	Asp	Leu	Leu
				35			40				45			

Ser	Cys	Leu	Ala	Val	Ser	Arg	Ile	Phe	Leu	Gln	Leu	Phe	Ile	Phe	Tyr
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Val	Asn	Val	Ile	Val	Ile	Phe	Phe	Ile	Glu	Phe	Ile	Met	Cys	Ser	Ala
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Asn	Cys	Ala	Ile	Leu	Leu	Phe	Ile	Asn	Glu	Leu	Glu	Leu	Trp	Leu	Ala
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Thr	Trp	Leu	Gly	Val	Phe	Tyr	Cys	Ala	Lys	Val	Ala	Ser	Val	Arg	His
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Pro	Leu	Phe	Ile	Trp	Leu	Lys	Met	Arg	Ile	Ser	Lys	Leu	Val	Pro	Trp
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Met	Ile	Leu	Gly	Ser	Leu	Leu	Tyr	Val	Ser	Met	Ile	Cys	Val	Phe	His
130					135				140						

Ser Lys Tyr Ala Gly Phe Met Val Pro Tyr Phe Leu Arg Lys Phe Phe
 145 150 155 160
 Ser Gln Asn Ala Thr Ile Gln Lys Glu Asp Thr Leu Ala Ile Gln Ile
 165 170 175
 Phe Ser Phe Val Ala Glu Phe Ser Val Pro Leu Leu Ile Phe Leu Phe
 180 185 190
 Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met
 195 200 205
 Arg Asn Thr Val Ala Gly Ser Arg Val Pro Gly Arg Gly Ala Pro Ile
 210 215 220
 Ser Ala Leu Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Phe Ser His
 225 230 235 240
 Cys Met Ile Lys Val Phe Leu Ser Ser Leu Lys Phe His Ile Arg Arg
 245 250 255
 Phe Ile Phe Leu Phe Phe Ile Leu Val Ile Gly Ile Tyr Pro Ser Gly
 260 265 270
 His Ser Leu Ile Leu Ile Leu Gly Asn Pro Lys Leu Lys Gln Asn Ala
 275 280 285
 Lys Lys Phe Leu Leu His Ser Lys Cys Cys Gln
 290 295

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<211> 900

<212> DNA

<213> Homo sapiens

<220>

<223> human T2R01 (hGR01)

<400> 2

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 atggctccgc tggatctcct tctttctgt ctggcagttt ctagaatttt tctgcagttg 180
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<212> PRT

<213> Homo sapiens

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<220>
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<222> (143)
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Cys Asn Glu Leu Ile Lys His Arg Lys Leu Met Pro Ile Gln Ile Leu
35 40 45

Leu Met Cys Ile Gly Met Ser Arg Phe Gly Leu Gln Met Val Leu Met
50 55 60

Val Gln Ser Phe Phe Ser Val Phe Phe Pro Leu Leu Tyr Val Lys Ile
65 70 75 80

Ile Tyr Gly Ala Ala Met Met Phe Leu Trp Met Phe Phe Ser Ser Ile
85 90 95

Ser Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
100 105 110

Ser Gly Phe Thr Gln Ser Cys Phe Leu Trp Leu Lys Phe Arg Ile Pro
115 120 125

Lys Leu Ile Pro Trp Leu Phe Trp Glu Ala Phe Trp Pro Leu Xaa Ala
130 135 140

Leu His Leu Cys Val Glu Val Asp Tyr Ala Lys Asn Val Glu Glu Asp
145 150 155 160

Ala Leu Arg Asn Thr Thr Leu Lys Lys Ser Lys Thr Lys Ile Lys Lys
165 170 175

Ile Ser Glu Val Leu Leu Val Asn Leu Ala Leu Ile Phe Pro Leu Ala
180 185 190

Ile Phe Val Met Cys Thr Ser Met Leu Leu Ile Ser Leu Tyr Lys His
195 200 205

Thr His Arg Met Gln His Gly Ser His Gly Phe Arg Asn Ala Asn Thr
210 215 220

Glu Ala His Ile Asn Ala Leu Lys Thr Val Ile Thr Phe Phe Cys Phe
225 230 235 240

Phe Ile Ser Tyr Phe Ala Ala Phe Met Thr Asn Met Thr Phe Ser Leu
245 250 255

Pro Tyr Arg Ser His Gln Phe Phe Met Leu Lys Asp Ile Met Ala Ala
260 265 270

Tyr Pro Ser Gly His Ser Val Ile Ile Ile Leu Ser Asn Ser Lys Phe
275 280 285

Gln Gln Ser Phe Arg Arg Ile Leu Cys Leu Lys Lys Lys Leu
290 295 300

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<212> DNA
<213> Homo sapiens

<220>
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<220>
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aagctaattgc caattcaaat cctcttaatg tgcataaggaa tgtcttagatt tggctctgcag 180
atgggtgttaa tggtacaaag tttttctct gtgttcttc cactcctta cgtcaaaata 240
atttatgggtt cagcaatgtt gttccttgg atgtttttt gctctatcag cctatggttt 300
gccacttggc tttctgtatt ttactgcctc aagatttcag gcttcactca gtcctgtttt 360
ctttgggttga aattcaggat cccaaagtttta ataccttggc tgcttctggg aagcgttctg 420
gcctctgtga gcattgcattc tggatgttgc ggttagattac gctaaaaatg tggaaagagga 480
tgccctcaga aacaccacac taaaaaaagag taaaacaaag ataaagaaaa ttatgtgaagt 540
gttcttggc aacttggcat taatatttcc tctagccata tttgtatgtt gcaattctat 600
gttactcatc tctctttaca agcacactca tcggatgttca catggatctc atggcttttag 660
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tcaccagttc tttatgttga aggacataat ggcagcatat ccctctggcc actcggttat 840
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<213> Homo sapiens

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<223> human T2R03 (hGR03)

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Ser Ser Trp Phe Lys Thr Lys Arg Met Ser Leu Ser Asp Phe Ile Ile
35 40 45

Thr Thr Leu Ala Leu Leu Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr
50 55 60

Asp Ser Phe Leu Ile Glu Phe Ser Pro Asn Thr His Asp Ser Gly Ile
65 70 75 80

Ile Met Gln Ile Ile Asp Val Ser Trp Thr Phe Thr Asn His Leu Ser
85 90 95

Ile Trp Leu Ala Thr Cys Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala
 100 105 110
 Ser Phe Ser His Pro Thr Phe Leu Trp Leu Lys Trp Arg Val Ser Arg
 115 120 125
 Val Met Val Trp Met Leu Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser
 130 135 140
 Thr Ala Ser Leu Ile Asn Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly
 145 150 155 160
 Ile Glu Ala Thr Arg Asn Val Thr Glu His Phe Arg Lys Lys Arg Ser
 165 170 175
 Glu Tyr Tyr Leu Ile His Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro
 180 185 190
 Leu Ile Val Ser Leu Ala Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly
 195 200 205
 Arg His Thr Arg Gln Met Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro
 210 215 220
 Thr Thr Glu Ala His Lys Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe
 225 230 235 240
 Phe Leu Phe Leu Leu Tyr Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly
 245 250 255
 Asn Phe Leu Pro Lys Thr Lys Met Ala Lys Met Ile Gly Glu Val Met
 260 265 270
 Thr Met Phe Tyr Pro Ala Gly His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285
 Ser Lys Leu Lys Gln Thr Phe Val Val Met Leu Arg Cys Glu Ser Gly
 290 295 300
 His Leu Lys Pro Gly Ser Lys Gly Pro Ile Phe Ser
 305 310 315

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 <212> DNA
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<220>
 <223> human T2R03 (hGR03)

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 tggtcaagt ggagagtttc tagggatgt gtatggatgc tggtgggtgc actgcttta 420
 tcctgtggta gtaccgcata tctgtatcaat gagtttaagc tctattctgt ctttagggga 480
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tctttgctca tcttctccct ggggaggcac acacggcaga tgctgaaaaa tgggacaagc 660
tccagagatc caaccactga ggcccacaag agggccatca gaatcatcct ttccttcttc 720
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aaaaccaaga tggctaagat gattggcgaa gtaatgacaa tgtttatcc tgctggccac 840
tcatttatttc tcattctggg gaacagtaag ctgaagcaga cattttagt gatgctccgg 900
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<212> PRT

<213> Homo sapiens

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<223> human T2R04 (hGR04)

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Lys Thr Trp Val Lys Ser His Arg Ile Ser Ser Ser Asp Arg Ile Leu
35 40 45

Phe Ser Leu Gly Ile Thr Arg Phe Leu Met Leu Gly Leu Phe Leu Val
50 55 60

Asn Thr Ile Tyr Phe Val Ser Ser Asn Thr Glu Arg Ser Val Tyr Leu
65 70 75 80

Ser Ala Phe Phe Val Leu Cys Phe Met Phe Leu Asp Ser Ser Val
85 90 95

Trp Phe Val Thr Leu Leu Asn Ile Leu Tyr Cys Val Lys Ile Thr Asn
100 105 110

Phe Gln His Ser Val Phe Leu Leu Leu Lys Arg Asn Ile Ser Pro Lys
115 120 125

Ile Pro Arg Leu Leu Ala Cys Val Leu Ile Ser Ala Phe Thr Thr
130 135 140

Cys Leu Tyr Ile Thr Leu Ser Gln Ala Ser Pro Phe Pro Glu Leu Val
145 150 155 160

Thr Thr Arg Asn Asn Thr Ser Phe Asn Ile Ser Glu Gly Ile Leu Ser
165 170 175

Leu Val Val Ser Leu Val Leu Ser Ser Ser Leu Gln Phe Ile Ile Asn
180 185 190

Val Thr Ser Ala Ser Leu Leu Ile His Ser Leu Arg Arg His Ile Gln
195 200 205

Lys Met Gln Lys Asn Ala Thr Gly Phe Trp Asn Pro Gln Thr Glu Ala
210 215 220

His Val Gly Ala Met Lys Leu Met Val Tyr Phe Leu Ile Leu Tyr Ile
225 230 235 240

Pro Tyr Ser Val Ala Thr Leu Val Gln Tyr Leu Pro Phe Tyr Ala Gly
245 250 255

Met Asp Met Gly Thr Lys Ser Ile Cys Leu Ile Phe Ala Thr Leu Tyr
260 265 270

Ser Pro Gly His Ser Val Leu Ile Ile Ile Thr His Pro Lys Leu Lys
275 280 285

Thr Thr Ala Lys Lys Ile Leu Cys Phe Lys Lys
290 295

<210> 8

<211> 900

<212> DNA

<213> Homo sapiens

<220>

<223> human T2R04 (hGR04)

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ctatttctgg tgaacaccat ctacttcgtc tcttcaaata cggaaaggc agtctacctg 240
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ctgaagcggg atatctcccc aaagatcccc aggctgctgc tggcctgtgt gctgatttct 420
gctttcacca cttgcctgtt catcacgtt agccaggcat cacctttcc tgaacttgg 480
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cactccttga ggagacatat acagaagatg cagaaaaatg ccactggtttt ctgaaatccc 660
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ccatatttgc ttgctaccctt ggtccagttt ctccctttt atgcaggat ggtatgggg 780
accaaatcca tttgtctgtat ttttgcacc ctttactctc caggacattc ttttctcatt 840
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<213> Homo sapiens

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20 25 30

Arg Glu Trp Ile Arg Lys Phe Asn Trp Ser Ser Tyr Asn Leu Ile Ile
35 40 45

Leu Gly Leu Ala Gly Cys Arg Phe Leu Leu Gln Trp Leu Ile Ile Leu
 50 55 60

Asp Leu Ser Leu Phe Pro Leu Phe Gln Ser Ser Arg Trp Leu Arg Tyr
 65 70 75 80

Leu Ser Ile Phe Trp Val Leu Val Ser Gln Ala Ser Leu Trp Phe Ala
 85 90 95

Thr Phe Leu Ser Val Phe Tyr Cys Lys Lys Ile Thr Thr Phe Asp Arg
 100 105 110

Pro Ala Tyr Leu Trp Leu Lys Gln Arg Ala Tyr Asn Leu Ser Leu Trp
 115 120 125

Cys Leu Leu Gly Tyr Phe Ile Ile Asn Leu Leu Leu Thr Val Gln Ile
 130 135 140

Gly Leu Thr Phe Tyr His Pro Pro Gln Gly Asn Ser Ser Ile Arg Tyr
 145 150 155 160

Pro Phe Glu Ser Trp Gln Tyr Leu Tyr Ala Phe Gln Leu Asn Ser Gly
 165 170 175

Ser Tyr Leu Pro Leu Val Val Phe Leu Val Ser Ser Gly Met Leu Ile
 180 185 190

Val Ser Leu Tyr Thr His His Lys Lys Met Lys Val His Ser Ala Gly
 195 200 205

Arg Arg Asp Val Arg Ala Lys Ala His Ile Thr Ala Leu Lys Ser Leu
 210 215 220

Gly Cys Phe Leu Leu His Leu Val Tyr Ile Met Ala Ser Pro Phe
 225 230 235 240

Ser Ile Thr Ser Lys Thr Tyr Pro Pro Asp Leu Thr Ser Val Phe Ile
 245 250 255

Trp Glu Thr Leu Met Ala Ala Tyr Pro Ser Leu His Ser Leu Ile Leu
 260 265 270

Ile Met Gly Ile Pro Arg Val Lys Gln Thr Cys Gln Lys Ile Leu Trp
 275 280 285

Lys Thr Val Cys Ala Arg Arg Cys Trp Gly Pro
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 tggcctcat ataacctcat tattcctggc ctggctggct gccgatttct cctgcagtgg 180

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 <213> Homo sapiens

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 <223> Xaa = any amino acid

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Phe Leu Ile Gly Leu Val Gly Asn Gly Val Pro Val Val Cys Ser Phe
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Arg Gly Trp Val Lys Lys Met Xaa Gly Val Pro Ile Asn Ser His Asp
 35 40 45

Ser Gly Lys Xaa Pro Leu Ser Pro Thr Gln Ala Asp His Val Gly His
 50 55 60

Lys Ser Val Ser Thr Phe Pro Glu Gln Trp Leu Ala Leu Leu Ser Xaa
 65 70 75 80

Cys Leu Arg Val Leu Val Ser Gln Ala Asn Met Xaa Phe Ala Thr Phe
 85 90 95

Phe Ser Gly Phe Cys Cys Met Glu Ile Met Thr Phe Val Xaa Xaa Xaa
 100 105 110

Xaa
 115 120 125

Xaa Leu Leu Val Ser Phe Lys Ile Thr Phe Tyr Phe Ser Ala Leu Val
 130 135 140

Gly Trp Thr Leu Xaa Lys Pro Leu Thr Gly Asn Ser Asn Ile Leu His
 145 150 155 160

Pro Ile Leu Asn Leu Leu Phe Leu Xaa Ile Ala Val Gln Xaa Arg Arg
 165 170 175

Leu Ile Ala Ile Cys Asp Val Ser Val Pro Leu Val Phe Leu Xaa Arg
180 185 190

His His Arg Lys Met Glu Asp His Thr Ala Val Arg Arg Arg Leu Lys
195 200 205

Pro Arg Xaa
210 215 220

Xaa Leu Tyr Met Val Ser Ala Leu Ala Arg His Phe Ser Met Thr Phe
225 230 235 240

Xaa Ser Pro Ser Asp Leu Thr Ile Leu Ala Ile Ser Ala Thr Leu Met
245 250 255

Ala Val Tyr Thr Ser Phe Pro Ser Ile Val Met Val Met Arg Asn Gln
260 265 270

Thr Cys Gln Arg Ile Leu Xaa Glu Met Ile Cys Thr Trp Lys Ser
275 280 285

<210> 12

<211> 823

<212> DNA

<213> Homo sapiens

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<223> human T2R07 (hGR07)

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catgttggac ataagtctgt ttccacttcc ccagagcagt ggttggctt actatctta 240
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ccctttaaaa acccttaaca gaaacagca acatcctgca tcccatatata aatctgttat 480
ttttatagat tgctgtccag tgaaggagac tgattgctat ttgtgatgtt tctgttccac 540
ttgtctttttt gtaaagacat cacaggaaga tggaggacca cacagctgca aggaggaggc 600
tcaaaccacaa gtcctcatcg ctctgaactt cccctttac atggttctg cttggccac 660
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actcatggct gtttataactt catttccgtc tattgtaatg gttatgagga atcagacttg 780
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<211> 318

<212> PRT

<213> Homo sapiens

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<223> human T2R07 (hGR07)

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20							25							30	
Met	Asp	Trp	Val	Lys	Lys	Arg	Lys	Ile	Ala	Ser	Ile	Asp	Leu	Ile	Leu
35							40							45	
Thr	Ser	Leu	Ala	Ile	Ser	Arg	Ile	Cys	Leu	Leu	Cys	Val	Ile	Leu	Leu
50							55						60		
Asp	Cys	Phe	Ile	Leu	Val	Leu	Tyr	Pro	Asp	Val	Tyr	Ala	Thr	Gly	Lys
65							70						75		80
Glu	Met	Arg	Ile	Ile	Asp	Phe	Phe	Trp	Thr	Leu	Thr	Asn	His	Leu	Ser
85									90					95	
Ile	Trp	Phe	Ala	Thr	Cys	Leu	Ser	Ile	Tyr	Tyr	Phe	Phe	Lys	Ile	Gly
100								105						110	
Asn	Phe	Phe	His	Pro	Leu	Phe	Leu	Trp	Met	Lys	Trp	Arg	Ile	Asp	Arg
115							120						125		
Val	Ile	Ser	Trp	Ile	Leu	Leu	Gly	Cys	Val	Val	Leu	Ser	Val	Phe	Ile
130							135						140		
Ser	Leu	Pro	Ala	Thr	Glu	Asn	Leu	Asn	Ala	Asp	Phe	Arg	Phe	Cys	Val
145							150						155		160
Lys	Ala	Lys	Arg	Lys	Thr	Asn	Leu	Thr	Trp	Ser	Cys	Arg	Val	Asn	Lys
165							170						175		
Thr	Gln	His	Ala	Ser	Thr	Lys	Leu	Phe	Leu	Asn	Leu	Ala	Thr	Leu	Leu
180							185						190		
Pro	Phe	Cys	Val	Cys	Leu	Met	Ser	Phe	Phe	Leu	Leu	Ile	Leu	Ser	Leu
195							200						205		
Arg	Arg	His	Ile	Arg	Arg	Met	Gln	Leu	Ser	Ala	Thr	Gly	Cys	Arg	Asp
210							215						220		
Pro	Ser	Thr	Glu	Ala	His	Val	Arg	Ala	Leu	Lys	Ala	Val	Ile	Ser	Phe
225							230						235		240
Leu	Leu	Leu	Phe	Ile	Ala	Tyr	Tyr	Leu	Ser	Phe	Leu	Ile	Ala	Thr	Ser
245							250						255		
Ser	Tyr	Phe	Met	Pro	Glu	Thr	Glu	Leu	Ala	Val	Ile	Phe	Gly	Glu	Ser
260							265						270		
Ile	Ala	Leu	Ile	Tyr	Pro	Ser	Ser	His	Ser	Phe	Ile	Leu	Ile	Leu	Gly
275							280						285		
Asn	Asn	Lys	Leu	Arg	His	Ala	Ser	Leu	Lys	Val	Ile	Trp	Lys	Val	Met
290							295						300		
Ser	Ile	Leu	Lys	Gly	Arg	Lys	Phe	Gln	Gln	His	Lys	Gln	Ile		
305							310						315		

<210> 14
 <211> 957
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human T2R07 (hGR07)

 <400> 14
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 atcttaggga atgcattcat tggattggta aactgcattgg actgggtcaa gaagaggaaa 120
 attgcctcca ttgatttaat cctcacaagt ctggccatat ccagaatttgc tctattgtgc 180
 gtaatactat tagattgttt tatattgggt ctatatccag atgtctatgc cactggtaaa 240
 gaaatgagaa tcattgactt cttctggaca ctaaccaatc atttaagtat ctggtttgc 300
 acctgcctca gcatttacta tttcttcagaat ataggtaatt tctttcaccc acttttcctc 360
 tggatgaagt ggagaattga cagggtgatt tcctggattc tactgggtg cgtggttctc 420
 tctgtgttta ttagccttcc agccactgag aatttgaacg ctgatttcag gttttgtgtg 480
 aaggcaaaaga gggaaaacaaa cttaacttgg agttgcagag taaataaaac tcaacatgct 540
 tctaccaagt tatttctcaa cctggcaacg ctgctccctt tttgtgtgt cctaatgtcc 600
 ttttcctct tgatcctctc cctgcggaga catatcaggc gaatgcagct cagtgcacaca 660
 gggtgcagag accccagcac agaagcccat gtgagagccc tgaaagctgt catttccttc 720
 ctttcctct ttatgccta ctatttgcctc ttttcatttgc ccacctccag ctactttatg 780
 ccagagacgg aatttagctgt gattttgggtagtccatag ctctaatactaa cccctcaagt 840
 cattcattta tcctaataact ggggaacaat aaattaagac atgcatctct aaaggtgatt 900
 tggaaaagtaa tgtctattct aaaaggaaga aaattccaaac aacataaaaca aatctga 957

<210> 15
 <211> 309
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human T2R08 (hGR08)

 <400> 15
 Met Phe Ser Pro Ala Asp Asn Ile Phe Ile Ile Leu Ile Thr Gly Glu
 1 5 10 15

 Phe Ile Leu Gly Ile Leu Gly Asn Gly Tyr Ile Ala Leu Val Asn Trp
 20 25 30

 Ile Asp Trp Ile Lys Lys Lys Ile Ser Thr Val Asp Tyr Ile Leu
 35 40 45

 Thr Asn Leu Val Ile Ala Arg Ile Cys Leu Ile Ser Val Met Val Val
 50 55 60

 Asn Gly Ile Val Ile Val Leu Asn Pro Asp Val Tyr Thr Lys Asn Lys
 65 70 75 80

 Gln Gln Ile Val Ile Phe Thr Phe Trp Thr Phe Ala Asn Tyr Leu Asn
 85 90 95

 Met Trp Ile Thr Thr Cys Leu Asn Val Phe Tyr Phe Leu Lys Ile Ala
 100 105 110

 Ser Ser Ser His Pro Leu Phe Leu Trp Leu Lys Trp Lys Ile Asp Met
 115 120 125

Val Val His Trp Ile Leu Leu Gly Cys Phe Ala Ile Ser Leu Leu Val
 130 135 140

 Ser Leu Ile Ala Ala Ile Val Leu Ser Cys Asp Tyr Arg Phe His Ala
 145 150 155 160

 Ile Ala Lys His Lys Arg Asn Ile Thr Glu Met Phe His Val Ser Lys
 165 170 175

 Ile Pro Tyr Phe Glu Pro Leu Thr Leu Phe Asn Leu Phe Ala Ile Val
 180 185 190

 Pro Phe Ile Val Ser Leu Ile Ser Phe Phe Leu Leu Val Arg Ser Leu
 195 200 205

 Trp Arg His Thr Lys Gln Ile Lys Leu Tyr Ala Thr Gly Ser Arg Asp
 210 215 220

 Pro Ser Thr Glu Val His Val Arg Ala Ile Lys Thr Met Thr Ser Phe
 225 230 235 240

 Ile Phe Phe Phe Phe Leu Tyr Tyr Ile Ser Ser Ile Leu Met Thr Phe
 245 250 255

 Ser Tyr Leu Met Thr Lys Tyr Lys Leu Ala Val Glu Phe Gly Glu Ile
 260 265 270

 Ala Ala Ile Leu Tyr Pro Leu Gly His Ser Leu Ile Leu Ile Val Leu
 275 280 285

 Asn Asn Lys Leu Arg Gln Thr Phe Val Arg Met Leu Thr Cys Arg Lys
 290 295 300

 Ile Ala Cys Met Ile
 305

<210> 16
 <211> 930
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human T2R08 (hGR08)

<400> 16
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 atttccacag ttgactacat ctttaccaat ttagttatcg ccagaatttg ttgtatcgt 180
 gtaatggttg taaatggcat tggatagta ctgaacccag atgtttatac aaaaaataaa 240
 caacagatac tcattttac cttctggaca tttgccaact acttaaatat gtggattacc 300
 acctgcctta atgtcttcta ttttctgaag atagccagtt cctctcatcc actttttctc 360
 tggctgaagt ggaaaattga tatggtggtg cactggatcc tgctggatg ctttgcatt 420
 tccttggatc tcagccttat agcagcaata gtactgagtt gtgattatag gtttcatgca 480
 attgccaaac ataaaagaaa cattactgaa atgttccatg tgagtaaaat accataactt 540
 gaacccttga ctctctttaa cctgtttgca attgtccat ttattgtgtc actgatatca 600
 tttttccttt tagtaagatc tttatggaga cataccaagc aaataaaaact ctatgctacc 660
 ggcagtagag accccagcac agaagttcat gtgagagcca taaaactat gacttcattt 720
 atcttctttt ttttcctata ctatatttct tctatgttgc tgaccttttag ctatctttag 780
 aaaaaataaca agttagctgt ggagtttggaa gagattgcag caattctcta ccccttgggt 840
 cactcactta ttttaattgt tttaaataat aaactgaggc agacatttgt cagaatgctg 900

acatgttagaa aaattgcctg catgatatga

930

<210> 17
<211> 312
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R09 (hGR09)

<400> 17
Met Pro Ser Ala Ile Glu Ala Ile Tyr Ile Ile Leu Ile Ala Gly Glu
1 5 10 15
Leu Thr Ile Gly Ile Trp Gly Asn Gly Phe Ile Val Leu Val Asn Cys
20 25 30
Ile Asp Trp Leu Lys Arg Arg Asp Ile Ser Leu Ile Asp Ile Ile Leu
35 40 45
Ile Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Ser Leu
50 55 60
Asp Gly Phe Phe Met Leu Leu Phe Pro Gly Thr Tyr Gly Asn Ser Val
65 70 75 80
Leu Val Ser Ile Val Asn Val Val Trp Thr Phe Ala Asn Asn Ser Ser
85 90 95
Leu Trp Phe Thr Ser Cys Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
100 105 110
Asn Ile Ser His Pro Phe Phe Trp Leu Lys Leu Lys Ile Asn Lys
115 120 125
Val Met Leu Ala Ile Leu Leu Gly Ser Phe Leu Ile Ser Leu Ile Ile
130 135 140
Ser Val Pro Lys Asn Asp Asp Met Trp Tyr His Leu Phe Lys Val Ser
145 150 155 160
His Glu Glu Asn Ile Thr Trp Lys Phe Lys Val Ser Lys Ile Pro Gly
165 170 175
Thr Phe Lys Gln Leu Thr Leu Asn Leu Gly Val Met Val Pro Phe Ile
180 185 190
Leu Cys Leu Ile Ser Phe Phe Leu Leu Leu Phe Ser Leu Val Arg His
195 200 205
Thr Lys Gln Ile Arg Leu His Ala Thr Gly Phe Arg Asp Pro Ser Thr
210 215 220
Glu Ala His Met Arg Ala Ile Lys Ala Val Ile Ile Phe Leu Leu Leu
225 230 235 240
Leu Ile Val Tyr Tyr Pro Val Phe Leu Val Met Thr Ser Ser Ala Leu
245 250 255

Ile Pro Gln Gly Lys Leu Val Leu Met Ile Gly Asp Ile Val Thr Val
260 265 270

Ile Phe Pro Ser Ser His Ser Phe Ile Leu Ile Met Gly Asn Ser Lys.
 . 275 . 280 . 285 .

Leu Arg Glu Ala Phe Leu Lys Met Leu Arg Phe Val Lys Cys Phe Leu
290 295 300

Arg Arg Arg Lys Pro Phe Val Pro
305 310

<210> 18
<211> 939
<212> DNA
<213> *Homo sapiens*

<220>
<223> human T2R09 (hGR09)

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<400> 18
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atttggggaa atggattcat tgtacttagtt aactgcattt actggctaa aagaagagat 120
atttccttga ttgacatcat cctgatcagc ttggccatct ccagaatctg tctgctgtgt 180
gtaatatcat tagatggctt ctttatgctg ctctttccag gtacatatgg caatagcgtg 240
ctagtaagca ttgtgaatgt tgtctggaca ttggccaata attcaagtct ctggtttact 300
tcttgcctca gtatcttcta tttaactcaag atagccaata tatgcacccc attttcttc 360
tggctgaagc taaagatcaa caaggtcatg ctgcgattt ttctggggtc ctttcttata 420
tctttaatta ttagtgttcc aaagaatgtat gatatgtgtt atcacctttt caaagtcaagt 480
catgaagaaa acattacttg gaaattcaaa gtggagtaaaa ttccaggtaac tttcaaaacag 540
ttaaccctga acctgggggt gatggttccc ttatcctt gcctgatctc attttcttg 600
ttacttttct cccttagtttag acacaccaag cagattcgac tgcatgtac agggttcaga 660
gacccccaga cagaggccca catgagggcc ataaaaggccat tgatcatctt tctgctctc 720
ctcatcggtt actacccaggat ctttctgtt atgacccatctt ggcgtctgtat tcctcaggaa 780
aaatttagtgt tgatgatttgg tgacatagta actgtcattt tcccatcaag ccattcattt 840
attctaatta tggaaatag caagttgagg gaagtttttca tgaagatgtt aagatttgg 900
aagtgtttcc tttagaagaagaa aagccctttt gttccatag 939

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<210> 19
<211> 307
<212> PRT
<213> *Homo sapiens*

<220>
<223> human T2R10 (hGR10)

<400> 19
Met Leu Arg Val Val Glu Gly Ile Phe Ile Phe Val Val Val Ser Glu
1 5 10 15

Ser Val Phe Gly Val Leu Gly Asn Gly Phe Ile Gly Leu Val Asn Cys
 20 25 30

Ile Asp Cys Ala Lys Asn Lys Leu Ser Thr Ile Gly Phe Ile Leu Thr
35 40 45

Gly Leu Ala Ile Ser Arg Ile Phe Leu Ile Trp Ile Ile Ile Thr Asp
50 55 60

Gly Phe Ile Gln Ile Phe Ser Pro Asn Ile Tyr Ala Ser Gly Asn Leu
65 70 75 80

Ile Glu Tyr Ile Ser Tyr Phe Trp Val Ile Gly Asn Gln Ser Ser Met
85 90 95

Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Tyr Ile Phe Leu Trp Leu Lys Ser Arg Thr Asn Met Val
115 120 125

Leu Pro Phe Met Ile Val Phe Leu Leu Ile Ser Ser Leu Leu Asn Phe
130 135 140

Ala Tyr Ile Ala Lys Ile Leu Asn Asp Tyr Lys Thr Lys Asn Asp Thr
145 150 155 160

Val Trp Asp Leu Asn Met Tyr Lys Ser Glu Tyr Phe Ile Lys Gln Ile
165 170 175

Leu Leu Asn Leu Gly Val Ile Phe Phe Thr Leu Ser Leu Ile Thr
180 185 190

Cys Ile Phe Leu Ile Ile Ser Leu Trp Arg His Asn Arg Gln Met Gln
195 200 205

Ser Asn Val Thr Gly Leu Arg Asp Ser Asn Thr Glu Ala His Val Lys
210 215 220

Ala Met Lys Val Leu Ile Ser Phe Ile Ile Leu Phe Ile Leu Tyr Phe
225 230 235 240

Ile Gly Met Ala Ile Glu Ile Ser Cys Phe Thr Val Arg Glu Asn Lys
245 250 255

Leu Leu Leu Met Phe Gly Met Thr Thr Thr Ala Ile Tyr Pro Trp Gly
260 265 270

His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Ala Ser
275 280 285

Leu Arg Val Leu Gln Gln Leu Lys Cys Cys Glu Lys Arg Lys Asn Leu
290 295 300

Arg Val Thr
305

<210> 20

<211> 924

<212> DNA

<213> Homo sapiens

<220>

<223> human T2R10 (hGR10)

<400> 20

atgctacgtg tagtggagg catttcatt tttgtttag tagtgagtc agtgggg 60
gtttgggg atggatttat tggacttcta aactgcattg actgtgccaa gaataagtt 120
tctacgattt gctttattct caccggctta gaattttct gatatggata 180

ataattacag atggatttat acagatattc tctccaaata tatatgcctc cggtAACCTA 240
attGAATATA ttGTTTACTT ttGGGTAATT ggtAAATCAAT caAGTATGTG gTTTGCACCC 300
agCCTCAGCA tCTTCTATT CCTGAAGATA gCAAATTTT CCAACTACAT ATTTCCTCTGG 360
ttGAAGAGCA gaACAAATAT gGTTCTTCCC TTCATGATAG TATTCTTACT TATTCTCATCG 420
ttACTTAATT ttGCAATACAT tGCAAGATT CTTAATGATT ATAAAACGAA gaATGACACAA 480
gtCTGGGATC tCAACATGTA tAAAAGTGAAT TACTTTTAAACAGATTTT GCTAAATCTG 540
ggAGTCATTt tCTTCTTAC ACTATCCCTA ATTACATGTA TTTTTTAAT CATTCCCTT 600
tggAGACACA acAGGCGAGAT gCAATCGAAAT GTGACAGGAT TGAGAGACTC CAACACAGAA 660
gCTCATGTGA aggCAATGAAAT AGTTTGATA TCTTCATCA TCCCTTTAT CTTGTATT 720
atAGGCAATGG CCATAGAAAT ATCATGTTT ACTGTGCGAG AAAACAAACT GCTGCTTATG 780
tttGGAATGA caACCACAGC CATCTATCCC TGGGGTCACT CATTATCTT AATTCTAGGA 840
aacAGCAAGC tAAAGCAAGC CTCTTGAGG GTACTGCAGC AATTGAAGTG CTGTGAGAAA 900
aggAAAAATC tcAGAGTCAC ATAG 924

<210> 21
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R11 (hGR11)

<220>
<221> MOD_RES
<222> (1)..(245)
<223> Xaa = any amino acid

<400> 21
Met Ala Asn Met Leu Lys Asn Met Leu Thr Met Ile Ser Ala Ile Asp
1 5 10 15

Phe Ile Met Gly Ile Gln Arg Ser Arg Val Val Met Val Leu Val His Cys
20 25 30

Ile Asp Trp Ile Arg Arg Trp Lys Leu Ser Leu Ile Asp Phe Ile Leu
35 40 45

Thr Cys Trp Ala Ile Ser Arg Ile Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Leu Cys Thr Xaa Phe
85 90 95

Ala Thr Cys Leu Ala Val Phe Tyr Phe Leu Lys Ile Val Asn Phe Ser
100 105 110

Tyr Leu Phe Tyr Phe Trp Leu Lys Trp Arg Ile Asn Lys Val Ala Phe
115 120 125

Ile Leu Pro Leu Val Ser Ala Phe Ser Val Tyr Gln Leu Ser Phe Asp
130 135 140

Val His Phe Xaa Cys Leu Leu Val Ser Cys Pro Lys Lys Tyr Glu Arg
145 150 155 160

His Met Thr Gly Leu Leu Asn Val Ser Asn Asn Lys Asn Val Asn Asn
165 170 175

Ile Ile Ile Phe Phe Ile Gly Ser Leu Ser Ser Phe Ser Ile Ser Ser
180 185 190

Ile Phe Phe Leu Leu Leu Leu Ser Ser Xaa Arg His Met Lys His
195 200 205

Ile Arg Phe Asn Phe Arg Asp Cys Arg Thr Pro Val Tyr Gly Pro Ile
210 215 220

Ser Glu Pro Arg Lys Arg Phe Ser Phe Phe Val Leu Leu Leu Tyr Lys
225 230 235 240

Asn Leu Pro Phe Ser
245

<210> 22

<211> 315

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R12 (hGR12)

<220>

<221> MOD_RES

<222> (1)..(315)

<223> Xaa = any amino acid

<400> 22

Met Ser Ser Ile Trp Glu Thr Leu Phe Ile Arg Ile Leu Val Val Xaa
1 5 10 15

Phe Ile Met Gly Thr Val Gly Asn Xaa Phe Ile Val Leu Val Asn Ile
20 25 30

Ile Asp Xaa Ile Arg Asn Xaa Lys Val Ser Leu Ile Asp Phe Ile Leu
35 40 45

Asn Cys Leu Ala Ile Ser Arg Ile Cys Phe Leu Xaa Ile Thr Ile Leu
50 55 60

Ala Thr Ser Phe Asn Ile Gly Tyr Glu Lys Met Pro Asp Ser Lys Asn
65 70 75 80

Leu Ala Val Ser Phe Asp Ile Leu Trp Thr Gly Ser Ser Tyr Phe Cys
85 90 95

Leu Ser Cys Thr Thr Cys Leu Ser Val Phe Tyr Phe Leu Lys Val Ala
100 105 110

Asn Phe Ser Asn Pro Ile Phe Leu Trp Met Lys Trp Lys Ile His Lys
115 120 125

Val Leu Leu Phe Ile Val Leu Glu Ala Thr Ile Ser Phe Cys Thr Thr
130 135 140

Ser Ile Leu Lys Glu Ile Ile Asn Ser Leu Ile Xaa Glu Arg Val
145 150 155 160

Thr Ile Lys Gly Asn Leu Thr Phe Asn Tyr Met Asp Thr Met His Asp
 165 170 175
 Phe Thr Ser Leu Phe Leu Leu Gln Met Met Phe Ile Leu Pro Phe Val
 180 185 190
 Glu Thr Leu Ala Ser Ile Leu Leu Ile Leu Ser Leu Trp Ser His
 195 200 205
 Thr Arg Gln Met Lys Leu His Gly Ile Tyr Ser Arg Asp Pro Ser Thr
 210 215 220
 Glu Ala His Val Lys Pro Ile Lys Ala Ile Ile Ser Phe Leu Leu Leu
 225 230 235 240
 Phe Ile Val His Tyr Phe Ile Ser Ile Ile Leu Thr Leu Ala Cys Pro
 245 250 255
 Leu Leu Asp Phe Val Ala Ala Arg Thr Phe Ser Ser Val Leu Val Phe
 260 265 270
 Phe His Pro Ser Gly His Ser Phe Leu Leu Ile Leu Arg Asp Ser Lys
 275 280 285
 Leu Lys Gln Ala Ser Leu Cys Val Leu Lys Lys Met Lys Tyr Ala Lys
 290 295 300
 Lys Asp Ile Ile Ser His Phe Tyr Lys His Ala
 305 310 315

<210> 23
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human T2R12 (hGR12)

<400> 23
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 actgtggaa attgattcat tgtattggtt aatatcattg actgaatcag gaactgaaag 120
 gtctccctga ttgattttat tctcaactgc ttggccatct ccaggatatg tttcctgttag 180
 ataacaatt tagctacctc tttcaatata ggctatgaga aaatgcctga ttctaaagaat 240
 cttgcagtaa gtttgacat tctctggaca ggatccagct atttctgcct gtccctgtacc 300
 acttgcctca gtgtcttcta tttcctcaag gtagccaact tctccaatcc cattttcctc 360
 tggatgaaat ggaaaattca caaggtgcct ctctttattg tactagaggc aacgatctct 420
 ttctgcacaa cttccattct gaaggaaata ataattaata gtttaatcta agaacggta 480
 acaataaaaag gcaacttgac atttaattat atggatacca tgcatgatt cacttctctg 540
 tttctcccttc agatgatgtt catccttcct tttgtggaaa cactggcttc catttctctc 600
 ttaatcctct ccttatggag ccacaccagg cagatgaagc tacatggat ttattccagg 660
 gatcccagca cagaagccca tgtaaaacct ataaaagcta taatttcatt tctactcctc 720
 ttattgtgc attatttcat cagtatcata ctaacattgg cctgtccctct tctagacttc 780
 gttgcggcaa ggacttttag tagtgtgcgtg gtattttcc atccatctgg ccattcattt 840
 ctcttaattt tacggacag caaactgaag caagttctc tctgtgcct gaagaagatg 900
 aagtatgcca aaaaggacat aatctctcat tttataaac atgcctga 948

<210> 24
<211> 303
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R13 (hGR13)

<400> 24
Met Glu Ser Ala Leu Pro Ser Ile Phe Thr Leu Val Ile Ile Ala Glu
1 5 10 15

Phe Ile Ile Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ile Asn Cys
20 25 30

Ile Asp Trp Val Ser Lys Arg Glu Leu Ser Ser Val Asp Lys Leu Leu
35 40 45

Ile Ile Leu Ala Ile Ser Arg Ile Gly Leu Ile Trp Glu Ile Leu Val
50 55 60

Ser Trp Phe Leu Ala Leu His Tyr Leu Ala Ile Phe Val Ser Gly Thr
65 70 75 80

Gly Leu Arg Ile Met Ile Phe Ser Trp Ile Val Ser Asn His Phe Asn
85 90 95

Leu Trp Leu Ala Thr Ile Phe Ser Ile Phe Tyr Leu Leu Lys Ile Ala
100 105 110

Ser Phe Ser Ser Pro Ala Phe Leu Tyr Leu Lys Trp Arg Val Asn Lys
115 120 125

Val Ile Leu Met Ile Leu Leu Gly Thr Leu Val Phe Leu Phe Leu Asn
130 135 140

Leu Ile Gln Ile Asn Met His Ile Lys Asp Trp Leu Asp Arg Tyr Glu
145 150 155 160

Arg Asn Thr Thr Trp Asn Phe Ser Met Ser Asp Phe Glu Thr Phe Ser
165 170 175

Val Ser Val Lys Phe Thr Met Thr Met Phe Ser Leu Thr Pro Phe Thr
180 185 190

Val Ala Phe Ile Ser Phe Leu Leu Ile Phe Ser Leu Gln Lys His
195 200 205

Leu Gln Lys Met Gln Leu Asn Tyr Lys Gly His Arg Asp Pro Arg Thr
210 215 220

Lys Val His Thr Asn Ala Leu Lys Ile Val Ile Ser Phe Leu Leu Phe
225 230 235 240

Tyr Ala Ser Phe Phe Leu Cys Val Leu Ile Ser Trp Ile Ser Glu Leu
245 250 255

Tyr Gln Asn Thr Val Ile Tyr Met Leu Cys Glu Thr Ile Gly Val Phe
260 265 270

Ser Pro Ser Ser His Ser Phe Leu Leu Ile Leu Gly Asn Ala Lys Leu
 275 280 285

Arg Gln Ala Phe Leu Leu Val Ala Ala Lys Val Trp Ala Lys Arg
290 295 300

<210> 25
<211> 912
<212> DNA
<213> *Homo sapiens*

<220>
<223> human T2R13 (hGR13)

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<400> 25
atggaaagtgcctgccgag tatcttcact cttgtataa ttgcagaatt cataattggg 60
aatttgagca atggatttat agtactgatc aactgcattt actgggtcag taaaagagag 120
ctgtccctcag tcgataaaact cctcattatc ttggcaatct ccagaattgg gctgatctgg 180
gaaatattag taagttgggt ttagtctcg cattatctag ccatatttgt gtctggaca 240
ggattaagaa ttatgatttt tagctggata gtttctaattc acttcaatct ctggcttgct 300
acaatcttca gcatctttt tttgctcaaa atagcgagtt tctcttagccc tgctttctc 360
tatttgaagt ggagagtaaa caaagtgtt ctgatgtatac tgcttaggaac ttggcttc 420
ttatTTTaa atctgataca aataaacatg catataaaag actggcttgg ccgatatgaa 480
agaaaacacaa ctggaaattt cagttatgtt gactttggaa cattttcagt gtcggctcaaa 540
ttcactatga ctatgttcag tctaacacca ttactgtgg ctttcatctc ttttctcctg 600
ttaattttct ccctgcagaa acatctccag aaaatgcac tcaattacaa aggacacaga 660
gaccccagga ccaagggtcca tacaaatgcc ttgaaaattt tgatcttcatt ctttttatttc 720
tatgctagtt ttttctatg tgttctata tcatggattt ctgagctgtt tcagaacaca 780
gtgatctaca tgctttgtga gacgattggg gtcttccttc cttcaagccca ctcctttctt 840
ctgattctag gaaaacgtttaa gttaaagacag gcctttctt tggggcagc taaggtatgg 900
qcttaaacgtt qaa

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<210> 26
<211> 317
<212> PRT
<213> *Homo sapiens*

<220>
<223> human T2R14 (hGR14)

<400> 26
Met Gly Gly Val Ile Lys Ser Ile Phe Thr Phe Val Leu Ile Val Glu
1 5 10 15

Phe Ile Ile Gly Asn Leu Gly Asn Ser Phe Ile Ala Leu Val Asn Cys
 20 25 30

Ile Asp Trp Val Lys Gly Arg Lys Ile Ser Ser Val Asp Arg Ile Leu
35 40 45

Thr Ala Leu Ala Ile Ser Arg Ile Ser Leu Val Trp Leu Ile Phe Gly
50 55 60

Ser Trp Cys Val Ser Val Phe Phe Pro Ala Leu Phe Ala Thr Glu Lys
 65 70 75 80

Met Phe Arg Met Leu Thr Asn Ile Trp Thr Val Ile Asn His Phe Ser
85 90 95

Val Trp Leu Ala Thr Gly Leu Gly Thr Phe Tyr Phe Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser Asn Ser Ile Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys
 115 120 125
 Val Val Leu Val Leu Leu Val Thr Ser Val Phe Leu Phe Leu Asn
 130 135 140
 Ile Ala Leu Ile Asn Ile His Ile Asn Ala Ser Ile Asn Gly Tyr Arg
 145 150 155 160
 Arg Asn Lys Thr Cys Ser Ser Asp Ser Ser Asn Phe Thr Arg Phe Ser
 165 170 175
 Ser Leu Ile Val Leu Thr Ser Thr Val Phe Ile Phe Ile Pro Phe Thr
 180 185 190
 Leu Ser Leu Ala Met Phe Leu Leu Ile Phe Ser Met Trp Lys His
 195 200 205
 Arg Lys Lys Met Gln His Thr Val Lys Ile Ser Gly Asp Ala Ser Thr
 210 215 220
 Lys Ala His Arg Gly Val Lys Ser Val Ile Thr Phe Phe Leu Leu Tyr
 225 230 235 240
 Ala Ile Phe Ser Leu Ser Phe Phe Ile Ser Val Trp Thr Ser Glu Arg
 245 250 255
 Leu Glu Glu Asn Leu Ile Ile Leu Ser Gln Val Met Gly Met Ala Tyr
 260 265 270
 Pro Ser Cys His Ser Cys Val Leu Ile Leu Gly Asn Lys Lys Leu Arg
 275 280 285
 Gln Ala Ser Leu Ser Val Leu Leu Trp Leu Arg Tyr Met Phe Lys Asp
 290 295 300
 Gly Glu Pro Ser Gly His Lys Glu Phe Arg Glu Ser Ser
 305 310 315

<210> 27
 <211> 954
 <212> DNA
 <213> Homo sapiens

<220>
 <223> huamn T2R14 (hGR14)

<400> 27
 atgggtggtg tcataaaagag catatttaca ttgcgtttaa ttgtggaatt tataattgga 60
 aatttaggaa atagttcat agcactggtg aactgtattg actgggtcaa gggaaagaaag 120
 atctcttcgg ttgatcgat cctcaactgt ttggcaatct ctcgaattag cctgggttgg 180
 ttaatattcg gaagctggtg tgtgtctgtg ttttcccgat ctttatttgc cactgaaaaa 240
 atgttcagaa tgcttactaa tatctggaca gtgatcaatc attttagtgt ctggtttagct 300
 acaggcctcg gtactttta ttttctcaag atagccaatt ttctcaactc tattttctc 360
 taccttaaagt ggagggtaa aaaggtggtt ttggtgctgc ttcttgac ttcggcttcc 420
 ttgtttttaa atattgcact gataaacatc catataaatg ccagtatcaa tggatacaga 480
 agaaaacaaga cttgcagttc tgattcaagt aactttcac gattttccag tcttattgta 540

ttaaccagca ctgtgttcat tttcataccc tttactttgt ccctggcaat gtttcttctc 600
 ctcatcttct ccatgtggaa acatcgcaag aagatgcagc acactgtcaa aatatccgga 660
 gacgccagca ccaaagccca cagaggagtt aaaagtgtga tcactttctt cctactctat 720
 gccatttctt ctctgtcttt tttcatatca gtttggacct ctgaaagggtt ggaggaaaat 780
 ctaattatcc ttcccaggt gatggaaatg gcttatacctt catgtcactc atgtgttctg 840
 attcttgaa acaagaagct gagacaggcc tctctgtcag tgctactgtg gctgaggtac 900
 atgttcaaag atggggagcc ctcaggtcac aaagaattta gagaatcatc ttga 954

<210> 28
 <211> 300
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R15 (hGR15)

<220>
 <221> MOD_RES
 <222> (257)
 <223> Xaa = any amino acid

<400> 28

Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Val Thr
 1 5 10 15

Phe Val Leu Gly Asn Phe Ala Asn Gly Phe Ile Val Leu Val Asn Ser
 20 25 30

Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60

His Trp Tyr Ala Thr Val Leu Asn Pro Gly Ser Tyr Ser Leu Gly Val
 65 70 75 80

Arg Ile Thr Thr Ile Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
 85 90 95

Trp Val Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Ile Lys Ser Val
 115 120 125

Ile Pro Val Ile Leu Leu Gly Ser Leu Leu Phe Leu Val Cys His Leu
 130 135 140

Val Val Val Asn Met Asp Glu Ser Met Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Ser Trp Glu Ile Lys Leu Ser Asp Pro Thr His Leu Ser Asp
 165 170 175

Met Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Leu Ser Phe Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Phe His Gly Lys Gly Ser Pro Asp Ser Asn Thr Lys Val His
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Phe Ala Val
225 230 235 240

Tyr Phe Leu Ser Leu Ile Thr Ser Ile Trp Asn Phe Arg Arg Arg Leu
245 250 255

Xaa Asn Glu Pro Val Leu Met Leu Ser Gln Thr Thr Ala Ile Ile Tyr
260 265 270

Pro Ser Phe His Ser Phe Ile Leu Ile Trp Gly Ser Lys Lys Leu Lys
275 280 285

Gln Thr Phe Leu Leu Ile Leu Cys Gln Ile Lys Cys
290 295 300

<210> 29
<211> 903
<212> DNA
<213> Homo sapiens

<220>
<223> human T2R15 (hGR15)

<400> 29
atgataacctt ttctacccat catttttcc attctagtag tggttacatt tggttttggg 60
aattttgcta atggcttcat agtgttgta aattccattt agtgggtcaa gagacaaaag 120
atctcccttg ctgaccaaattt tctcaactgtt ctggcagtctt ccagaggttgg tttgctctgg 180
gttatattat tacatttgta tgcaactgtt ttgaatccag gttcatatag tttaggagta 240
agaattacta ctattaatgc ctgggctgtt accaaccattt tcagcatctg ggttgctact 300
agcctcagca tatttttattt cctcaagattt gccaattttt ccaactttat ttttcttcac 360
ttaaaaaagga gaattaagag tgcatttcca gtgataactat tggggctttt gtatttttt 420
gtttgtcattt ttgttggta aaacatggat gagagtatgtt ggacaaaaga atatgaagga 480
aacgtgagttt gggagatcaa attgagtgtt ccgacgcacc tttcagatat gactgtaacc 540
acgcttgcaa acttaataacc cttaactctg tccctgttat cttttctgtt ctaatctgt 600
tctttgttta aacatctcaa gaagatgcag ttccatggca aaggatctcc agattccaaac 660
accaagggtcc acataaaaagc ttgcatttccgtt gtgaccttcc ttctctgtt atttgcgtt 720
tactttctgtt cccttaatcac atcgatttgg aatttttagga ggaggctgtt gaaacgaaacc 780
gtcctctatgc tcagccaaac tactgcaattt atataccctt catttcatttcc attcatccta 840
atttggggaa gcaagaagctt gaaacagacc tttcttttga ttttgcgttca gattaagtgc 900
tga 903

<210> 30
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R16 (hGR16)

<400> 30
Met Ile Pro Ile Gln Leu Thr Val Phe Phe Met Ile Ile Tyr Val Leu
1 5 10 15

Glu Ser Leu Thr Ile Ile Val Gln Ser Ser Leu Ile Val Ala Val Leu
20 25 30

Gly Arg Glu Trp Leu Gln Val Arg Arg Leu Met Pro Val Asp Met Ile
 35 40 45

Leu Ile Ser Leu Gly Ile Ser Arg Phe Cys Leu Gln Trp Ala Ser Met
 50 55 60

Leu Asn Asn Phe Cys Ser Tyr Phe Asn Leu Asn Tyr Val Leu Cys Asn
 65 70 75 80

Leu Thr Ile Thr Trp Glu Phe Phe Asn Ile Leu Thr Phe Trp Leu Asn
 85 90 95

Ser Leu Leu Thr Val Phe Tyr Cys Ile Lys Val Ser Ser Phe Thr His
 100 105 110

His Ile Phe Leu Trp Leu Arg Trp Arg Ile Leu Arg Leu Phe Pro Trp
 115 120 125

Ile Leu Leu Gly Ser Leu Met Ile Thr Cys Val Thr Ile Ile Pro Ser
 130 135 140

Ala Ile Gly Asn Tyr Ile Gln Ile Gln Leu Leu Thr Met Glu His Leu
 145 150 155 160

Pro Arg Asn Ser Thr Val Thr Asp Lys Leu Glu Asn Phe His Gln Tyr
 165 170 175

Gln Phe Gln Ala His Thr Val Ala Leu Val Ile Pro Phe Ile Leu Phe
 180 185 190

Leu Ala Ser Thr Ile Phe Leu Met Ala Ser Leu Thr Lys Gln Ile Gln
 195 200 205

His His Ser Thr Gly His Cys Asn Pro Ser Met Lys Ala Arg Phe Thr
 210 215 220

Ala Leu Arg Ser Leu Ala Val Leu Phe Ile Val Phe Thr Ser Tyr Phe
 225 230 235 240

Leu Thr Ile Leu Ile Thr Ile Ile Gly Thr Leu Phe Asp Lys Arg Cys
 245 250 255

Trp Leu Trp Val Trp Glu Ala Phe Val Tyr Ala Phe Ile Leu Met His
 260 265 270

Ser Thr Ser Leu Met Leu Ser Ser Pro Thr Leu Lys Arg Ile Leu Lys
 275 280 285

Gly Lys Cys
 290

<210> 31
 <211> 876
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human T2R16 (hGR16)

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<400> 31
atgataccca tccaaactcac tgccttc atgatcatct atgtgcttga gtccttgaca 60
attattgtgc agagcagcct aattgttgc gtcgtggca gagaatggct gcaagtcaga 120
aggctgatgc ctgtggacat gattctcatc agcctggca tctctcgctt ctgtctacag 180
tgggcataaa tgctgaacaa ttttgcctc tattttatt tgaattatgt actttgcaac 240
ttaacaatca cctggaaatt ttttaatattt cttacattct ggttaaacag cttgcttacc 300
gtgttctact gcatcaaggct ctcttcattt accatcaca tcttctctg gctgagggtgg 360
agaattttga ggttgtttcc ctggatatta ctgggttctc tgatgattac ttgtgttaaca 420
atcatccctt cagctattgg gaattacatt caaattcagt tactcaccat ggagcatcta 480
ccaagaaaaca gcactgtaac tgacaaaactt gaaaattttc atcagtatca gttccaggct 540
catacagttt cattggttat tccttcattc ctgttccctgg cctccaccat ctttctcatg 600
gcatcaactga ccaagcagat acaacatcat agcaactggc actgcaatcc aagcatgaaa 660
gcgcgccttca ctgccttgag gtcccttgcc gtcttattta ttgtgtttac ctcttacttt 720
ctaaccatcat tcattcaccat tataggtaact ctatggata agagatgttg gttatgggtc 780
tgggaagctt ttgtctatgc ttcatctta atgcattcca cttcactgtat gctgagcagc 840
cctacgttga aaaggattct aaaggaaaag tgctag 876

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<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

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<220>
<223> human T2R17 (hGR17)

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<220>
<221> MOD_RES
<222> (1)..(330)
<223> Xaa = any amino acid

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<400> 32
Met Cys Ser Ala Xaa Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe
1 5 10 15

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Ala Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Ile Asn
20 25 30

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Val Asn Asp Trp Val Lys Thr Gln Lys Ile Ser Ser Thr Asp Gln Ile
35 40 45

```

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Val Thr Ala Leu Ala Phe Ser Arg Ile Gly Leu Leu Xaa Thr Leu Ile
50 55 60

```

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Ile Leu Leu His Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Ser
65 70 75 80

```

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Leu Glu Val Arg Ile Val Pro Ser Asn Val Ser Ala Ile Ile Asn His
85 90 95

```

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Phe Ser Ile Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Phe Lys
100 105 110

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Ile Ala Asn Phe Ser Asn Phe Ile Phe Leu His Leu Lys Lys Arg Ile
115 120 125

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Lys Ser Val Leu Leu Val Ile Leu Leu Gly Ser Leu Val Phe Leu Ile
130 135 140

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Cys Asn Leu Ala Val Val Thr Met Asp Asp Ser Val Trp Thr Lys Glu
145 150 155 160

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Phe Glu Gly Asn Val Thr Trp Lys Ile Glu Leu Arg Asn Ala Ile His
 165 170 175
 Leu Ser Asn Met Thr Ile Thr Asn His Ala Ser Lys Leu His Thr Val
 180 185 190
 His Ser Asp Ser Asn Ile Phe Ser Ala Val Ser Leu Phe Ser Xaa Thr
 195 200 205
 Met Leu Ala Asn Phe Thr Leu Phe Ile Leu Thr Leu Ile Ser Phe Leu
 210 215 220
 Leu Leu Val Cys Ser Pro Cys Lys His Leu Lys Met Met Gln Leu His
 225 230 235 240
 Gly Lys Gly Ser Gln Asp Leu Ser Thr Lys Val His Ile Lys Pro Leu
 245 250 255
 Gln Thr Val Ile Ser Phe Arg Met Leu Phe Ala Ile Tyr Phe Leu Cys
 260 265 270
 Ile Ile Thr Ser Thr Trp Asn Pro Arg Thr Gln Gln Ser Asn Leu Val
 275 280 285
 Phe Leu Leu Tyr Gln Thr Leu Ala Ile Met Tyr Pro Ser Phe His Ser
 290 295 300
 Phe Ile Leu Ile Met Arg Ser Arg Lys Leu Lys Gln Thr Ser Leu Ser
 305 310 315 320
 Val Leu Cys Gln Val Thr Cys Trp Val Lys
 325 330

<210> 33
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R18 (hGR18)

<220>
 <221> MOD_RES
 <222> (98)
 <223> Xaa = any amino acid

<400> 33
 Met Phe Val Gly Ile Asn Ile Phe Phe Leu Val Val Ala Thr Arg Gly
 1 5 10 15
 Leu Val Leu Gly Met Leu Gly Asn Gly Leu Ile Gly Leu Val Asn Cys
 20 25 30
 Ile Glu Trp Ala Lys Ser Trp Lys Val Ser Ser Ala Asp Phe Ile Leu
 35 40 45
 Thr Ser Leu Ala Ile Val Arg Ile Ile Arg Leu Tyr Leu Ile Leu Phe
 50 55 60

Asp Ser Phe Ile Met Val Leu Ser Pro His Leu Tyr Thr Ile Arg Lys
 65 70 75 80
 Leu Val Lys Leu Phe Thr Ile Leu Trp Ala Leu Ile Asn Gln Leu Ser
 85 90 95
 Ile Xaa Phe Ala Thr Cys Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser His Ser Leu Phe Leu Trp Leu Lys Trp Arg Met Asn Gly
 115 120 125
 Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp
 130 135 140
 Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp
 145 150 155 160
 Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp
 165 170 175
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Tyr Val Ile Pro
 180 185 190
 Phe Leu Leu Thr Leu Thr Ser Leu Leu Leu Phe Ile Ser Leu Val
 195 200 205
 Arg His Thr Lys Asn Leu Gln Leu Asn Ser Leu Gly Ser Arg Asp Ser
 210 215 220
 Ser Thr Glu Ala His Lys Arg Ala Met Lys Met Val Ile Ala Phe Leu
 225 230 235 240
 Leu Leu Phe Ile Ile Asn Phe Ile Ser Thr Leu Ile Gly Asp Trp Ile
 245 250 255
 Phe Leu Glu Val Glu Asn Tyr Gln Val Met Met Phe Ile Met Met Ile
 260 265 270
 Leu Leu Ala Phe Pro Ser Gly His Ser Phe Ile Ile Leu Gly Asn
 275 280 285
 Asn Lys Leu Arg Gln Ser Ser Leu Arg Leu Leu Trp His Leu Lys Phe
 290 295 300
 Ser Leu Lys Lys Ala Lys Pro Leu Thr Ser
 305 310

<210> 34
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human T2R18 (hGR18)

<400> 34
 atgttcgttg gaatttaatat tttctttctg gtgggtggcaa caagaggact tgtcttagga 60
 atgctggaaa acgggctcat tggactggta aactgcattg agtgggccaa gagttggaag 120
 gtctcatcag ctgatttcat cctcaccacgc ttggctatag tcagaatcat tcgactgtat 180

ttaatactat ttgattcatt tataatggta ttgtccccctc atctatatac catccgtaaa 240
 ctagtaaaac tgtttactat tctttggca ttaattaatc agttaagtat ctagttgcc 300
 acctgcctaa gcattttcta cttgcttaag atagccaatt tctcccactc cctttcctc 360
 tggctgaagt ggagaatgaa cggaatgatt gttatgcttc ttatattgtc tttgttctta 420
 ctgatttttgc acagtttagt gctagaataaaa tttattgtata tctcactcaa tataatagat 480
 aaaagtaatc tgactttata ttttagatgaa agtaaaaactc tctatgataa actctctatt 540
 ttaaaaaactc ttctcagctt gacatacgtt attccctttc ttctgactct gacctctttg 600
 ctccttttat ttatatcctt agtgagacac accaagaatt tgcagctcaa ctctctggc 660
 tcaaggact ccagcacaga ggcccataaa agggccatga aaatgggtat agccttcctc 720
 ctccctttta ttattaaactt tatttccact ttaataggag attggatctt ccttgaggtt 780
 gagaattatc aggtcatgtat gtttattatg atgattttac ttgccttcc ctcaggccac 840
 tcattttata taattttggg aaacaacaag ctaagacaga gctccttgag actactgtgg 900
 catcttaaat tctctctgaa aaaagcaaaa cctttaactt catag 945

<210> 35
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R19 (hGR19)

<400> 35
 Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu Ile Cys
 1 5 10 15

Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys Met Arg
 20 25 30

Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile Lys
 35 40 45

Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile Tyr Phe
 50 55 60

Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln Ser Lys
 65 70 75 80

Leu Val Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro Ser Phe
 85 90 95

His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln Thr Phe
 100 105 110

Leu Ser Val Leu Trp Gln Met Thr Cys
 115 120

<210> 36
 <211> 466
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human T2R19 (hGR19)

<400> 36
 ctgttaactac tctagcaaac ctcataccct ttactctgag cctaataatgt tttctgctgt 60
 taatctgttc tctttgtaaa catctcaaga agatgcggct ccatagcaaa ggatctcaag 120
 atcccagcac caaggccat ataaaagctt tgcaaactgt gaccccttc ctcatgttat 180

ttgccattta ctttctgtgt ataatcacat caacttgaa tcttaggaca cagcagagca 240
aacttgtact cctgcttgc caaactgttgc caatcatgtt tccttcattt cactcattttca 300
tcctgattat gggaaagttagg aagctaaaac agacctttct ttcagtttg tggcagatga 360
catgctgagt gaaagaagag aaaccctcaa ctccatagat tcacaagggg agcatcgtgg 420
gtcttctagc agaaaaacaaa ctgatggtgt ctggAACATT ttatat 466

<210> 37
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R20 (hGR20)

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

<400> 37
His Leu Xaa Arg Lys Ala Lys Ser Val Val Leu Val Ile Val Leu Gly
1 5 10 15

Ser Leu Phe Phe Leu Val Cys Gln Leu Val Met Lys Asn Thr Tyr Ile
20 25 30

Asn Val Trp Thr Glu Glu Cys Glu Gly Asn Val Thr Trp Lys Ile Lys
35 40 45

Leu Arg Asn Ala Met His Leu Ser Asn Leu Thr Val Ala Met Leu Ala
50 55 60

Asn Leu Ile Pro Phe Thr Leu Thr Val Ile Ser Phe Leu Leu Ile
65 70 75 80

Tyr Ser Leu Cys Lys His Leu Lys Lys Met Gln Leu His Gly Lys Gly
85 90 95

Ser Gln Asp Pro Ser Thr Lys Ile His Ile Lys Ala Leu Gln Thr Val
100 105 110

Thr Ser Phe Leu Val Leu Leu Ala Ile Tyr Phe Leu Cys Leu Ile Ile
115 120 125

Ser

<210> 38
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<223> human T2R20 (hGR20)

<220>
<221> modified_base
<222> (12)
<223> n = g, a, c or t

<400> 38
 ttcatcaattt anaaaaggaag gctaaggatg tagttctggat gatagtgttgggggtctttgt 60
 tcttttttgtt ttgtcaactt gtgatgaaaaa acacgtatataatgtgtgg acagaagaat 120
 gtgaaggaaaaa cgtaacctgg aagatcaaacc tgaggaatgc aatgcaccc ttccaaacttga 180
 ctgttagccat gctagcaaac ttgataccat tcactctgac cgtgatatact tttctgtgt 240
 taatctactc tctgtgtaaa catctgaaga agatgcagct ccatggcaaa ggatctcaag 300
 atcccagcac caagatccac ataaaagctc tgccaaactgt gaccccttc ctcgtattac 360
 ttgccattta ctttctgtgt ctaatcatat ccttttg 397

<210> 39
 <211> 312
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R21 (hGR21)

<220>
 <221> MOD_RES
 <222> (1)..(312)
 <223> Xaa = any amino acid

<400> 39
 Met Pro Pro Gly Ile Gly Asn Thr Phe Leu Ile Val Met Met Gly Glu
 1 5 10 15

Phe Ile Ile Xaa Met Leu Gly Asn Gly Phe Ile Val Leu Val Asn Cys
 20 25 30

Ile Asp Trp Xaa Gly Val Lys Xaa Ser Tyr Xaa Thr Thr Ala Ser Ser
 35 40 45

Pro Ala Trp Leu Ser Pro Gln Ser Val Asn Phe Gly Xaa Tyr Tyr Leu
 50 55 60

Ile His Leu Xaa Gln His Tyr Gly His Ile Tyr Met Pro Ser Ile Asn
 65 70 75 80

Xaa Xaa Asn Leu Phe Ile Phe Phe Gly His Xaa Pro Ile Thr Xaa Leu
 85 90 95

Pro Gly Leu Leu Pro Xaa Cys Phe Leu Leu Leu Xaa Asn Thr Tyr Phe
 100 105 110

Ser His Pro Cys Phe Ile Trp Leu Arg Trp Arg Ile Ser Arg Thr Leu
 115 120 125

Leu Glu Leu Pro Leu Gly Ser Leu Leu Leu Phe Phe Asn Leu Ala
 130 135 140

Leu Thr Gly Gly Leu Ser Asp Leu Trp Ile Asn Ile Tyr Thr Ile Tyr
 145 150 155 160

Glu Arg Asn Ser Thr Trp Ser Leu Asp Val Ser Lys Ile Leu Tyr Cys
 165 170 175

Ser Leu Trp Ile Leu Val Ser Leu Ile Tyr Leu Ile Ser Phe Leu Leu
 180 185 190

Ser Leu Ile Ser Leu Leu Leu Ile Leu Ser Leu Met Arg His Ile
195 200 205

Arg Asn Leu Gln Leu Asn Thr Met Gly Pro Arg Asp Leu Arg Met Lys
210 215 220

Ala His Lys Arg Ala Met Lys Met Lys Met Met Val Ser Phe
225 230 235 240

Leu Leu Phe Phe Leu Val His Phe Ser Ser Leu Leu Pro Thr Gly Trp
245 250 255

Ile Phe Leu Ile Gln Gln Lys Xaa Gln Ala Asn Phe Phe Val Leu Leu
260 265 270

Thr Ser Ile Ile Phe Pro Ser Ser His Ser Phe Val Leu Ile Leu Glu
275 280 285

Asn Cys Lys Leu Arg Gln Thr Ala Val Gly Pro Leu Trp His Leu Lys
290 295 300

Cys His Leu Lys Arg Val Lys Leu
305 310

<210> 40

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R22 (hGR22)

<220>

<221> MOD_RES

<222> (1)..(90)

<223> Xaa = any amino acid

<400> 40

Met Ala Thr Glu Ser Asp Thr Asn Leu Leu Ile Leu Ala Ile Ala Glu
1 5 10 15

Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys
20 25 30

Ser Glu Xaa Ile Lys Asn Xaa Lys Val Phe Ser Ala Asp Phe Ile Leu
35 40 45

Thr Cys Leu Ala Ile Ser His Asn Gly Gln Leu Leu Val Ile Leu Phe
50 55 60

Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg
65 70 75 80

Leu Xaa Lys Asn Cys Ile Met Leu Trp Thr
85 90

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<210> 41
<211> 656
<212> DNA
<213> Homo sapiens

<220>
<223> human T2R22 (hGR22)

<220>
<221> modified_base
<222> (1)..(656)
<223> n = g, a, c or t

<400> 41
tatagggacn gtgatgcttc gtacactctc caagaagaaa cactccgtga ggtatgtgag 60
actgcatncc ttagtagatc tnttgggata tatattcata atatagaaaa anaggcaaag 120
acttncttaa gtatatgaga ctctatccaa cagcagaagg ttctgatcaa gactggaagt 180
gcaatanaag caatgaagat aagtatcaga tatgaatgct cttctgcaat ggtctgattg 240
tnacattatt aatgatacan agtattaaa acttggattt tnttgcctt ggagatggcc 300
acccaatcg acacaaatct tctgattctg gcaatagcag aattcatcat cagcatgctg 360
ggaatgtgt tcattggact ggtaaactgc tctgaangga tcaagaacca naaggcttc 420
tcagctgact tcattccac ctgcttgct atctctcaca atggacaaact gttggtgata 480
ctgtttgatt catttctagt gggacttgct tcacatctat ataccacata tagactanga 540
aaaaactgtta ttatgctttg gacatgacta atcaacttgac acactgcttc gcacgtgcta 600
gcattttctca ttcttagata gccacttcnc actccttgtc tctgctgaag tggat 656

<210> 42
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R23 (hGR23)

<220>
<221> MOD_RES
<222> (1)..(72)
<223> Xaa = any amino acid

<400> 42
Val Ala Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Val
1 5 10 15

Asn Val Ile Asp Xaa Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln
20 25 30

Ile Leu Thr Ala Leu Val Val Ser Arg Ile Gly Xaa Thr Leu Xaa His
35 40 45

Ser Ile Pro Xaa Asp Ala Thr Arg Cys Xaa Ser Ala Leu Tyr Arg Xaa
50 55 60

Glu Val Arg Ile Val Ala Ser Asn
65 70

<210> 43
<211> 589
<212> DNA
<213> Homo sapiens

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<220>
<223> human T2R23 (hGR23)

<220>
<221> modified_base
<222> (1)..(589)
<223> n = g, a, c or t

<400> 43
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gagaatgtat atgaagagga gtgaatttga gtcgtttga gaataatgac cttttctatt 120
tctataaaaga cagtttggaa ttcatctatt agcatatgct ggtgcttgc tggtgacact 180
agtcaactgaa tttaaaggca gaaaatgtt a tgcacattt agtaatcaag tggtcatcga 240
agttaacatc tggatgttaa aggactcaga acaagtgtt a tgaaggcctgc atttttttat 300
ctgttcaaac atgatgtgtt ntctgctcat catttcatca attctggtag agttgcattt 360
gttcttggaa atgtngccaa tggcttcata gctctagtaa atgtcattga ctgngttaac 420
acacgaaaga tctcctcagc tgagcaaatt ctcaactgctc tggtggtctc cagaattgg 480
intactctgn gtcatagtagat tccttgagat gcaactagat gttaatctgc tctatataagg 540
ntagaagtaa gaattgttgc ttctaatgcc tgagctcgta cgaaccatt 589

<210> 44
<211> 314
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R24 (hGR24)

<400> 44
Met Ala Thr Glu Leu Asp Lys Ile Phe Leu Ile Leu Ala Ile Ala Glu
 1           5           10          15

Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys
 20          25           30

Ser Glu Gly Ile Lys Asn Gln Lys Val Phe Ser Ala Asp Phe Ile Leu
 35          40          45

Thr Cys Leu Ala Ile Ser Thr Ile Gly Gln Leu Leu Val Ile Leu Phe
 50          55          60

Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg
 65          70          75          80

Leu Gly Lys Thr Val Ile Met Leu Trp His Met Thr Asn His Leu Thr
 85          90          95

Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
100         105         110

His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly
115         120         125

Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp
130         135         140

Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp
145         150         155         160

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Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp
 165 170 175
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro
 180 185 190
 Phe Ser Leu Phe Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val
 195 200 205
 Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser
 210 215 220
 Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu
 225 230 235 240
 Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Gly Ile
 245 250 255
 Phe Phe Met Leu Trp Asn Asn Lys Tyr Ile Lys Phe Val Met Leu Ala
 260 265 270
 Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285
 Ser Lys Leu Arg Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn
 290 295 300
 Tyr Thr Lys Thr Pro Asn Ala Leu Pro Leu
 305 310

<210> 45
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human T2R24 (hGR24)

<400> 45
 atggccaccc aattggacaa aatctttctg attctggcaa tagcagaatt catcatcagc 60
 atgctgggaa atgtgttcat tggactggta aactgctctg aaggatcaa gaacaaaaag 120
 gtcttcttag ctgacttcat ctcacatgc ttgctatct ccacaattgg acaactgttg 180
 gtgatactgt ttgattcatt tctagtgaaa cttgcttcac atttatatac cacatataga 240
 ctagaaaaaa ctgttattat gcttggcac atgactaatac acttgacaac ctggcttgcc 300
 acctgcctaa gcattttcta tttctttaag atagcccact tcccccaactc cttttccctc 360
 tggctgagggt ggaggatgaa cggaatgatt gttatgcttc ttatattgtc tttgttctta 420
 ctgatttttg acagtttagt gctagaata tttattgata tctcactcaa tataatagat 480
 aaaagtaatc tgactttata ttttagatgaa agtaaaactc tctatgataa actctctatt 540
 ttaaaaactc ttctcagctt aaccagtttt atcccccttt ctctgttccct gaccccttg 600
 ctttttttat ttctgtccctt ggtgagacat actagaaatt tgaagctcag ttccttgggc 660
 tctagagact ccagcacaga gggccatagg agggccatga aaatgggtat gtctttccctt 720
 ttcccttctca tagttcattt tttttcctta caagtggcca atggatatt ttttatgttg 780
 tggacaaca agtacataaaa gtttgcatg ttagccttaa atgccttcc ctcgtgccac 840
 tcatttattc tcatttctggg aaacagcaag ctgcgacaga cagctgtgag gctactgtgg 900
 catcttagga actatacaaa aacaccaaat gctttacctt tgttag 945

<210> 46
 <211> 72
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human T2R25 (hGR25)

 <400> 46
 Leu Ser Pro Phe Arg Met Leu Phe Ala Ile Tyr Phe Leu Cys Ile Ile
 1 5 10 15

 Thr Ser Thr Trp Asn Pro Arg Thr Gln Gln Ser Asn Leu Val Phe Leu
 20 25 30

 Leu Tyr Gln Thr Leu Ala Ile Met Tyr Pro Ser Phe His Ser Phe Ile
 35 40 45

 Leu Ile Met Arg Ser Arg Lys Leu Lys Gln Thr Ser Leu Ser Val Leu
 50 55 60

 Cys Gln Val Thr Cys Trp Val Lys
 65 70

<210> 47
 <211> 264
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human T2R26 (hGR26)

 <220>
 <221> MOD_RES
 <222> (20)
 <223> Xaa = any amino acid

 <400> 47
 Met Pro Pro Gly Ile Gly Asn Thr Phe Leu Ile Val Met Met Gly Glu
 1 5 10 15

 Phe Ile Ile Xaa Met Leu Gly Asn Gly Phe Ile Val Leu Val Asn Cys
 20 25 30

 Ile Asp Val Arg Ser Gln Met Ile Leu Leu Asp Asn Cys Ile Leu Thr
 35 40 45

 Ser Leu Ala Ile Ser Thr Ile Ser Gln Leu Trp Ile Ile Leu Leu Asp
 50 55 60

 Ser Phe Val Thr Ala Leu Trp Pro His Leu Tyr Ala Phe Asn Lys Leu
 65 70 75 80

 Ile Lys Phe Ile His Ile Phe Trp Ala Leu Thr Asn His Leu Val Thr
 85 90 95

 Trp Leu Ala Cys Cys Leu Ser Val Phe Tyr Phe Phe Lys Ile Ala Tyr
 100 105 110

Phe Ser His Pro Cys Phe Ile Trp Leu Arg Trp Arg Ile Ser Arg Thr
 115 120 125
 Leu Leu Glu Leu Pro Leu Gly Ser Leu Leu Leu Phe Phe Asn Leu
 130 135 140
 Ala Leu Thr Gly Gly Leu Ser Asp Leu Trp Ile Asn Ile Tyr Thr Met
 145 150 155 160
 Tyr Glu Arg Asn Ser Thr Trp Ser Leu Asp Val Ser Lys Ile Leu Tyr
 165 170 175
 Cys Ser Leu Trp Ile Leu Val Ser Leu Ile Tyr Leu Ile Ser Phe Leu
 180 185 190
 Leu Ser Leu Ile Ser Leu Leu Leu Ile Leu Ser Leu Met Arg His
 195 200 205
 Ile Arg Asn Leu Gln Leu Asn Thr Met Gly Pro Arg Asp Leu Arg Met
 210 215 220
 Lys Ala His Lys Arg Ala Met Lys Met Lys Met Met Val Ser
 225 230 235 240
 Phe Leu Leu Phe Phe Leu Val His Phe Ser Ser Leu Leu Pro Thr Gly
 245 250 255
 Trp Ile Phe Leu Ile Gln Gln Lys
 260

<210> 48
 <211> 264
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R27 (hGR27)

<220>
 <221> MOD_RES
 <222> (1)..(264)
 <223> Xaa = any amino acid

<400> 48
 Leu Ala Asn Leu Ile Asp Trp Ala Glu Asn Gln Ile Cys Leu Met Asp
 1 5 10 15

Phe Ile Leu Ser Ser Leu Ala Ile Cys Arg Thr Leu Leu Leu Gly Cys
 20 25 30

Cys Val Ala Ile Arg Cys Thr Tyr Asn Asp Tyr Pro Asn Ile Asp Ala
 35 40 45

Val Asn His Asn Leu Ile Lys Ile Ile Thr Ile Phe Asp Ile Leu Arg
 50 55 60

Leu Val Ser Lys Xaa Leu Gly Ile Trp Phe Ala Ser Tyr Leu Ser Ile
 65 70 75 80

Phe	Tyr	Leu	Leu	Lys	Val	Ala	Leu	Phe	His	His	Ala	Ile	Phe	Leu	Trp
							85				90				95
Leu	Lys	Trp	Arg	Ile	Ser	Arg	Ala	Val	Phe	Thr	Phe	Leu	Met	Ile	Phe
							100			105				110	
Leu	Phe	Phe	Tyr	Ile	Ser	Ile	Ile	Ser	Met	Ile	Lys	Ile	Lys	Leu	Phe
							115			120				125	
Leu	Asp	Gln	Cys	Xaa	Tyr	Lys	Ile	Xaa	Glu	Lys	Leu	Leu	Leu	Glu	Gly
							130			135				140	
Arg	Cys	Glu	Xaa	Ser	Pro	Pro	Ser	Cys	Xaa	Pro	Asp	Ala	His	Xaa	Pro
							145			150				155	
Gly	Val	Val	Tyr	Ser	Leu	Tyr	His	Phe	Ser	Tyr	Leu	Met	Phe	Leu	Val
							165			170				175	
Cys	Tyr	Leu	Pro	Lys	Gly	Lys	His	Cys	Thr	Ala	Val	Val	Ile	Gly	Asp
							180			185				190	
Trp	Leu	Gln	Arg	Pro	Arg	Thr	Glu	Ala	Tyr	Val	Arg	Ala	Met	Asn	Ile
							195			200				205	
Met	Ile	Ala	Phe	Phe	Phe	His	Leu	Leu	Tyr	Ser	Leu	Gly	Thr	Ser	Leu
							210			215				220	
Ser	Ser	Val	Ser	Tyr	Phe	Leu	Cys	Lys	Arg	Lys	Ile	Val	Ala	Leu	Gly
							225			230				235	
Ala	Tyr	Leu	Ser	Tyr	Pro	Leu	Ser	His	Ser	Phe	Ile	Leu	Ile	Met	Glu
							245			250				255	
Asn	Asn	Lys	Val	Arg	Lys	Ala	Leu								
							260								

<210> 49
<211> 35
<212> PRT
<213> *Homo sapiens*

<220>
<223> human T2R28 (hGR28)

<400> 49
Asn Ile Cys Val Leu Leu Ile Ile Leu Ser Ile Leu Val Val Ser Ala
1 5 10 15

Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Ile Asn Val
 20 25 30

Asn Asp Trp
35

<210> 50
<211> 36
<212> PRT
<213> *Homo sapiens*

<220>
<223> human T2R29 (hGR29)

<400> 50
Met Gln Ala Ala Leu Thr Ala Phe Phe Val Leu Leu Phe Ser Leu Leu
1 5 10 15

Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
20 25 30

Lys Glu Trp Leu
35

<210> 51
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R30 (hGR30)

<400> 51
Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Val Thr
1 5 10 15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Ser
20 25 30

Ile Glu Trp Val Lys Thr Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu
35 40 45

Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
50 55 60

His Trp Tyr Ala Asn Val Phe Asn Ser Ala Leu Tyr Ser Ser Glu Val
65 70 75 80

Gly Ala Val Ala Ser Asn Ile Ser Ala Ile Ile Asn His Phe Ser Ile
85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Arg Ser Val
115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
130 135 140

Ala Val Ile Thr Met Asp Asp Ser Val Trp Thr Lys Glu Tyr Glu Gly
145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn
165 170 175

Met Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Ile Leu Thr Leu
180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
225 230 235 240

Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu
245 250 255

Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro
260 265 270

Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
275 280 285

Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp Arg
290 295 300

Ser Leu Arg Leu His Arg Phe Thr Arg Gly Ala Leu Cys Val Phe
305 310 315

<210> 52

<211> 960

<212> DNA

<213> Homo sapiens

<220>

<223> human T2R30 (hGR30)

<400> 52

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aatttttcca atggcttcat agctctagta aattccattt gatgggtcaa gacacgaaag 120
atctccctcag ctgaccaaattt cctcaactgt ctgtgggtctt ccagagggtgg tttactctgg 180
gtcatattat tacattggta tgcaaatgtt tttatattttt ctttatatacg ttcagaagta 240
ggagctgttg cttctaatat ctcagcaataat atcaaccattt tcagcatctg gcttgcatact 300
agcctcagca tatttttattt gctcaagattt gccaattttt ccaacccattt ttttctccac 360
ttttaagaaga gaatttggat ttgtgttctg gtgatactgt tgggtccctt ggtatttttg 420
atttgtatc ttgctgtat aaccatggat gacagtgtgtt ggacaaaaga atatgaagga 480
aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaaatat gactgtaaac 540
acactagcaa acctcataacc cttcattctg acctaataat gttttctgtt gttatctgt 600
tctctgtgtt aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccac 660
accaagggtcc acataaaagc tttgcaact gtgacccctt ttcttctgtt atgtgccatt 720
tacatttctgtt ccatgatcat atcagttttt aattttggaa ggctggaaaa gcaacctgtc 780
ttcatgtttt gccaagctat tatattcagc tatttttttccaa cccacccattt catcctgatt 840
ttgggaaaca agaagctaaa gcagatttt ttttccatgtt tgcggcatgtt gaggtactgg 900
gtgaaagaca gaagccttcg tctccataga ttcacaagag gggcattgtt tgccttctgtt 960

<210> 53

<211> 299

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R31 (hGR31)

<220>

<221> MOD_RES

<222> (1)..(299)

<223> Xaa = any amino acid

<400> 53
 Met Thr Thr Phe Ile Pro Ile Ile Phe Ser Ser Val Val Val Val Leu
 1 5 10 15
 Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30
 Ile Glu Arg Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60
 Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
 65 70 75 80
 Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
 130 135 140
 Phe Val Ile Asn Met Lys Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Xaa
 165 170 175
 Met Thr Val Thr Ile Gly Ala Xaa Leu Val Pro Phe Thr Leu Ser Leu
 180 185 190
 Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Cys Ala Ile
 225 230 235 240
 Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
 245 250 255
 Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
 260 265 270
 Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
 275 280 285
 Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
 290 295

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<210> 54
<211> 900
<212> DNA
<213> Homo sapiens

<220>
<223> human T2R31 (hGR31)

<220>
<221> modified_base
<222> (1)..(900)
<223> n = g, a, c or t

<400> 54
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atctcttttgc tgaccaggat tctcaactgtcttggcggcttgc ccagagttgg tttgctctgg 180
gtattattat taaaattggta ttcaactgttcaatccag ctttttatag tgtagaagta 240
agaactactg cttataatgt ctgggcagta accggccatt tcagcaactg gcttgctact 300
gccttcagca tatttttattt gctcaagatt gccaatttctt ccaacccattt ttttcttcac 360
ttaaagagaga gagtaagag tgcattctgtgtatgtctgtt tggggcctttt actattttg 420
gcttgcacac ttttgcgtat aaacatgaaa gagattgtac ggacaaaaga atttgaagga 480
aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcanatat gactgtacc 540
attggagcan acttagtacc ctttactctgttccctgatat cttttctgtat gctaattctgt 600
tctctgtgtat aacatctcaa gaagatgcag ctcctatggag aaggatcgca agatctcagc 660
accaagggtcc acataaaagc tttgcaact ctgatctcttccat tccctctgtt atgtgccatt 720
ttctttcttat tcctaatcgtt tcgggttgg agtcccttagga ggctgcggaa tgacccgggtt 780
gtcatggtta gcaaggctgtt gggaaacata tatcttgcatt tcgactcattt catcctaattt 840
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<210> 55
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R32 (hGR32)

<400> 55
His Ser Phe Met Leu Thr Met Gly Ser Arg Lys Pro Lys Gln Thr Phe
1 5 10 15

Leu Ser Ala Leu
20

<210> 56
<211> 309
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R33 (hGR33)

<400> 56
Met Val Tyr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Phe Ala
1 5 10 15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val
20 25 30

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Ile Asp Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60

His Trp Tyr Ala Asn Val Phe Asn Ser Ala Leu Tyr Ser Leu Glu Val
 65 70 75 80

Arg Ile Val Ala Ser Asn Ile Ser Ala Val Ile Asn His Phe Ser Ile
 85 90 95

Trp Leu Ala Ala Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Lys Ser Val
 115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
 130 135 140

Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Met Leu Cys Ala Ile
 225 230 235 240

Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Asn Leu Arg Ser Leu Glu
 245 250 255

Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270

Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Phe Trp Gln Val Arg Tyr Trp Val Lys Gly Glu
 290 295 300

Lys Pro Ser Ser Pro
 305

<210> 57
 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
<223> human T2R33 (hGR33)

<400> 57

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atctcctcag ctgacccaaat tctactgtctgggtct ccagagttgg tttactctgg 180
gtcatattat tacattggta tgcaaattgtttaattcag ctttatatagtttttaga 240
agaattgttgcgttataat ctcagcagta atcaaccatttcagcatctg gcttgctgt 300
agcctcagca tatttttattt gctcaagatttgcatttccatccaaacccat 360
ctaaagaaga gaattaaagag tggttgcgtgtgttgcattttccatccaaacccat 420
atttgcatttgcgtgtatccatggat gagagagtgtgttgcattttccatccaaacccat 480
aatgtgactt ggaagatcaa atttgcatttgcgtgtgttgcattttccatccaaacccat 540
actctagccaa acctcatacc ctttactctg agcttaatatttttgcattttccatccaaacccat 600
tctcttgcataatctcaaa gaagatgcag ctccatagca aaggatctca agatcccagc 660
accaagggtcc acataaaaagc tttgcatttgcgtgtgttgcattttccatccaaacccat 720
tactttctgttgcatttgcgtgtgttgcatttgcgtgtgttgcattttccatccaaacccat 780
ttcatgttctgcatttgcgtgtgttgcatttgcgtgtgttgcattttccatccaaacccat 840
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gtgaaaggag agaaggccttcatccatccaaacccat 930

<210> 58
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R34 (hGR34)

<220>
<221> MOD_RES
<222> (1)..(100)
<223> Xaa = any amino acid

<400> 58

Gly Ser Ser Arg Xaa Lys Pro Pro Arg Ile Pro His Lys Lys Leu Cys
1 5 10 15

Lys Leu Gly Pro Ser Phe Pro His Asn Asn Leu Pro Ile Tyr Phe Leu
20 25 30

Cys Xaa Asn His Ile Val Leu Glu Phe Leu Lys Met Arg Pro Lys Lys
35 40 45

Lys Cys Ser Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro Ser
50 55 60

Phe His Ser Phe Ile Leu Xaa Trp Gly Asn Lys Thr Leu Lys Gln Thr
65 70 75 80

Phe Leu Ser Val Xaa Trp Gln Val Thr Cys Trp Ala Lys Gly Gln Asn
85 90 95

Gln Ser Thr Pro
100

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<210> 59
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R35 (hGR35)

<220>
<221> MOD_RES
<222> (1)..(128)
<223> Xaa = any amino acid

<400> 59
Asn Ala Ile Arg Pro Ser Lys Leu Trp Thr Val Thr Glu Ala Asp Lys
 1           5           10           15

Thr Ser Gln Pro Gly Thr Ser Ala Asn Lys Ile Phe Ser Ala Gly Asn
 20          25           30

Leu Ile Ser His Val Asn Met Ser Arg Arg Met Gln Leu His Gly Lys
 35          40           45

Gly Ser Gln His Leu Ser Thr Arg Val His Ile Lys Ala Xaa Gln Thr
 50          55           60

Val Ile Ser Phe Leu Met Leu Xaa Ala Ile Tyr Phe Leu Cys Leu Ile
 65          70           75           80

Thr Ser Thr Trp Asn Pro Arg Thr Gln Gln Ser Lys Leu Val Phe Leu
 85          90           95

Leu Tyr Gln Thr Leu Gly Phe Met Tyr Leu Leu Phe His Ser Phe Ile
100          105          110

Leu Thr Met Gly Ser Arg Lys Pro Lys Gln Thr Phe Leu Ser Ala Leu
115          120          125

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<210> 60
<211> 309
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R36 (hGR36)

<400> 60
Met Ile Cys Phe Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe Ala
 1           5           10           15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val
 20          25           30

Ile Asp Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35          40           45

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Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60

His Trp Tyr Ser Asn Val Leu Asn Ser Ala Leu Tyr Ser Ser Glu Val
 65 70 75 80

Ile Ile Phe Ile Ser Asn Ala Trp Ala Ile Ile Asn His Phe Ser Ile
 85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
 100 105 110

Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
 115 120 125

Val Leu Val Ile Val Leu Gly Pro Leu Val Phe Leu Val Cys His Leu
 130 135 140

Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn
 165 170 175

Leu Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
 180 185 190

Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240

Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu
 245 250 255

Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro
 260 265 270

Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Ile Phe Leu Ser Val Phe Trp Gln Met Arg Tyr Trp Val Lys Gly Glu
 290 295 300

Lys Pro Ser Ser Pro
 305

<210> 61
 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human T2R36 (hGR36)

<400> 61
 atgatatgtt ttctgctcat catttatca attctggtag tgttgcatt tgttcttgg 60
 aattttcca atggcttcat agctctagta aatgtcattg actgggtcaa gagacaaaag 120
 atctcctcaag ctgaccaaat cctcaactgct ctgggtgtct ccagagttgg ttactctgg 180
 gtaatattat tacattgta ttcaaatgtg ttgaatttag ctttatatacg ttcaagaatg 240
 ataattttta ttctaatgc ctggcaata atcaaccatt tcagcatcg gcttgctact 300
 agcctcagca tattttattt gctcaagatc gtcaatttct ccagacttat tttcatcac 360
 ttaaaaaggaa aggctaagag ttagttctg gtgatagtgt tgggtccctt ggtatttttg 420
 gtttgcacc ttgtgatgaa acacacgtat ataaatgtgt ggacaaaaga atatgaagga 480
 aatgtgactt ggaagatcaa actgaggaat gcaatacacc tttcaaaactt gactgtaaagc 540
 acactagcaa acttgatacc ctgcactctg accctgatcat cttttctgt gttaatctac 600
 tctctgtgtaa acatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660
 accaagggtcc acataaaaagc tttgcaaaact gtgacctctt ttcttctgtt atgtgccatt 720
 tacttctgtt ccatgatcat atcagttgtt aattttggaa ggctggaaaa gcaacctgtc 780
 ttcatgttctt gccaagctat tatattcagc tattttcaa cccaccattt catcctgatt 840
 ttgggaaaca agaagctaaa gcagatttt cttcagttt tttggcaaat gaggtactgg 900
 gtgaaaggag agaaggcttc atctccatag 930

<210> 62
 <211> 309
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R37 (hGR37)

<220>
 <221> MOD_RES
 <222> (1)..(309)
 <223> Xaa = any amino acid

<400> 62
 Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
 1 5 10 15
 Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30
 Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ser
 35 40 45
 His Cys Ser Gly Gly Val Gln Asn Trp Phe Thr Leu Gly His Ile Ile
 50 55 60
 Thr Leu Val Cys Asn Cys Val Xaa Phe Gly Phe Ile Xaa Ile Arg Ser
 65 70 75 80
 Lys Asn Phe Trp Phe Xaa Cys Leu Ser Asn Asn Gln Ala Phe Gln His
 85 90 95
 Val Gly Val Thr Ser Leu Ser Ile Phe His Leu Leu Lys Thr Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Lys Ser Val
 115 120 125
 Gly Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Phe Ile Cys Asn Leu
 130 135 140

Phe Val Ile Asn Met Asp Glu Ser Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Val Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr His Ser Asn
 165 170 175
 Met Thr Leu Thr Met Leu Ala Asn Phe Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Leu Gly Arg Leu Glu
 245 250 255
 Lys Gln Pro Val Phe Met Phe Cys Glu Ala Ile Ile Phe Ser Tyr Pro
 260 265 270
 Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Gly Glu
 290 295 300
 Lys Pro Ser Ser Ser
 305

<210> 63
 <211> 930
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human T2R37 (hGR37)

<400> 63
 atgataactt ttctgccat catttttcc attctaatag tggttacatt tgtgattgga 60
 aattttgcta atggcttcat agctctagta aattccattg agtgggttaa gagacaaaag 120
 atctcatcag ctgaccaaattt ttctcaactgc tctgggttg tccagaattt gtttactctg 180
 ggtcatattt ttacatttgtt atgcactgtt gtttattttt gcttcatata gattagaagt 240
 aagaattttt ggttctaattt tctcagcaat aaccaagcat ttcagcatgt ggtgttact 300
 agcctcagca tatttcattt gctcaagact gccaattttt ccaacccat ttttctccac 360
 ctaaagaaga ggattaagag tgggttttgg tggataactat tggggccctt gctattttc 420
 attttaatc tttttgttat aaacatggat gagagtgtat ggacaaaaga atatgaagga 480
 aacgtgactt ggaagatcaa attgaggagt gcaatgtacc attcaaataat gactctaacc 540
 atgcttagcaa actttgtacc cttcaactctg accctgatat cttttctgtt gttaatctgt 600
 tctctgttta aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660
 accaagggtcc acataaaaagc tttgcaact gtgacccctt ttcttctgtt atgtgccatt 720
 tactttctgtt ccatgatcat atcagtttgc aatttgggaa ggctggaaaa gcaacctgtc 780
 ttcatgttctt gcgaaagctat tatattcagc tatttttcaaa cccacccatt catcctgatt 840
 ttgggaaaca agaagctaaa gcagattttt ctttcagttt tgccggcatgt gaggtactgg 900
 gtgaaaggag agaaggccatc atcttcataag 930

<210> 64
 <211> 144
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R38 (hGR38)

<400> 64
 Met Leu Thr Leu Thr Arg Ile Arg Thr Val Ser Tyr Glu Val Arg Ser
 1 5 10 15

Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr
 20 25 30

Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
 35 40 45

Pro Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
 50 55 60

Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
 65 70 75 80

Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
 85 90 95

Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
 100 105 110

Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
 115 120 125

Leu Ile Cys Leu Ala Ser Trp Ser Pro Gly Arg Ser Pro Val Pro Ser
 130 135 140

<210> 65
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R39 (hGR39)

<400> 65
 Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val Arg Asn
 1 5 10 15

Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Leu Pro Leu Ser Val
 20 25 30

Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys His Met
 35 40 45

His Trp Met Gln Ser Glu Ser His Lys Leu Ser Ser Ala Arg Thr Glu
 50 55 60

Ala His Ile Asn Ala Leu Lys Thr Val Thr Phe Phe Cys Phe Phe
65 70 75 80

Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg Ile Pro
85 90 95

Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala Ala Tyr
100 105 110

Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys Phe Lys
115 120 125

Asp Leu Phe Arg Arg Met Ile Cys Leu Gln Lys Glu
130 135 140

<210> 66

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R40 (hGR40)

<400> 66

Ser Gln Tyr Ser Leu Gly His Ser Tyr Val Val Ile Phe Gly Tyr Gly
1 5 10 15

Gln Met Lys Lys Thr Phe Leu Gly Ile Leu Trp His Leu Lys Cys Gly
20 25 30

Leu Lys Gly Arg Ala Leu Leu Ala Thr Gln Val Gly Leu Arg Glu Lys
35 40 45

Ser Thr Arg Ser Leu Gly Val Ile Phe Leu Ala Ser Ser Tyr Ser Phe
50 55 60

Phe Val Tyr Val Leu Cys His
65 70

<210> 67

<211> 309

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R41 (hGR41)

<220>

<221> MOD_RES

<222> (253)

<223> Xaa = any amino acid

<400> 67

Met Ile Thr Phe Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe Ala
1 5 10 15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val
20 25 30

Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60
 His Trp Tyr Ala Asn Val Leu Asn Pro Ala Leu Tyr Ser Ser Glu Val
 65 70 75 80
 Ile Ile Phe Ile Ser Asn Ile Ser Ala Ile Ile Asn His Phe Ser Ile
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
 100 105 110
 Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
 115 120 125
 Val Leu Val Ile Val Leu Gly Pro Leu Val Phe Leu Val Cys His Leu
 130 135 140
 Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn
 165 170 175
 Leu Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240
 Tyr Phe Leu Tyr Leu Ile Thr Ser Thr Trp Asn Leu Xaa Thr Gln Gln
 245 250 255
 Ser Lys Leu Val Phe Met Phe Cys Gln Thr Leu Gly Ile Met Tyr Pro
 260 265 270
 Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Leu Cys Gln Val Thr Cys Leu Val Lys Gly Gln
 290 295 300
 Gln Pro Ser Thr Pro
 305

<210> 68
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
<223> human T2R42 (hGR42)

<400> 68
Phe Ile Gly Leu Thr Asp Cys Ile Ala Trp Met Arg Asn Gln Lys Leu
1 5 10 15
Cys Met Val Gly Phe Ile Leu Thr Arg Met Ala Leu Ala Arg Ile Asn
20 25 30
Ile Leu

<210> 69
<211> 297
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R43 (hGR43)

<220>
<221> MOD_RES
<222> (1)..(297)
<223> Xaa = any amino acid

<400> 69
Leu Glu Leu Ile Phe Ser Xaa Lys Val Val Ala Thr Arg Gly Leu Val
1 5 10 15
Leu Gly Met Leu Gly Asn Gly Leu Ile Gly Leu Val Asn Cys Ile Glu
20 25 30
Trp Ala Lys Ser Trp Lys Val Ser Ser Ala Asp Phe Ile Leu Thr Ser
35 40 45
Leu Ala Ile Val Arg Ile Ile Arg Leu Tyr Leu Ile Leu Phe Asp Ser
50 55 60
Phe Ile Met Val Leu Ser Pro His Leu Tyr Thr Xaa Xaa Xaa Xaa Xaa
65 70 75 80
Xaa
85 90 95
Xaa Xaa Ser Leu Ser Ile Phe His Trp Phe Lys Thr Ala Asn Phe Ser
100 105 110
Asn Leu Ile Phe Leu Pro Leu Lys Glu Asp Xaa Asn Val Trp Leu
115 120 125
Gly Asp Ala Val Gly Ala Leu Gly Ile Phe His Leu Xaa Ser Cys Ser
130 135 140
Glu Asn His Gly Xaa Glu Val Cys Gly Gln Lys Asn Met Lys Glu Phe
145 150 155 160
Cys Ser Gly Met Ile Lys Leu Arg Asn Ala Ile Gln Leu Ser Asn Leu
165 170 175

Thr Val Thr Met Pro Ala Asn Val Thr Pro Cys Thr Leu Thr Leu Ile
 180 185 190
 Ser Phe Leu Leu Leu Ile Tyr Ser Pro Cys Lys His Val Lys Lys Met
 195 200 205
 Gln Leu His Gly Lys Gly Ser Gln His Leu Ser Thr Lys Val His Ile
 210 215 220
 Lys Val Leu Gln Thr Val Ile Ser Phe Phe Leu Leu Cys Ala Ile Tyr
 225 230 235 240
 Phe Val Ser Val Ile Ile Ser Val Trp Ser Phe Lys Asn Leu Glu Asn
 245 250 255
 Lys Pro Val Phe Met Phe Cys Gln Ala Ile Gly Phe Ser Cys Ser Ser
 260 265 270
 Ala His Pro Phe Ile Leu Thr Met Gly Asn Lys Lys Leu Lys Gln Thr
 275 280 285
 Tyr Leu Ser Val Leu Trp Gln Met Arg
 290 295

<210> 70
 <211> 319
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R44 (hGR44)

<400> 70
 Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Ile
 1 5 10 15
 Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30
 Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Val Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60
 His Trp Tyr Ala Thr Gln Leu Asn Pro Ala Phe Tyr Ser Val Glu Val
 65 70 75 80
 Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Thr Asn His Phe Ser Ser
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Met Phe Tyr Leu Leu Arg Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu Arg Ile Lys Arg Arg Val Lys Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
 130 135 140

Phe	Val	Ile	Asn	Met	Asp	Glu	Thr	Val	Trp	Thr	Lys	Glu	Tyr	Glu	Gly
145					150					155				160	
Asn	Val	Thr	Trp	Lys	Ile	Lys	Leu	Arg	Ser	Ala	Met	Tyr	His	Ser	Asn
				165				170				175			
Met	Thr	Leu	Thr	Met	Leu	Ala	Asn	Phe	Val	Pro	Leu	Thr	Leu	Thr	Leu
				180				185				190			
Ile	Ser	Phe	Leu	Leu	Leu	Ile	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys
	195				200						205				
Met	Gln	Leu	His	Gly	Lys	Gly	Ser	Gln	Asp	Pro	Ser	Thr	Lys	Val	His
	210				215						220				
Ile	Lys	Ala	Leu	Gln	Thr	Val	Thr	Ser	Phe	Leu	Leu	Cys	Ala	Ile	
225				230				235				240			
Tyr	Phe	Leu	Ser	Met	Ile	Ile	Ser	Val	Cys	Asn	Leu	Gly	Arg	Leu	Glu
	245					250						255			
Lys	Gln	Pro	Val	Phe	Met	Phe	Cys	Gln	Ala	Ile	Ile	Phe	Ser	Tyr	Pro
	260				265						270				
Ser	Thr	His	Pro	Phe	Ile	Leu	Ile	Leu	Gly	Asn	Lys	Lys	Leu	Lys	Gln
	275				280						285				
Ile	Phe	Leu	Ser	Val	Leu	Arg	His	Val	Arg	Tyr	Trp	Val	Lys	Asp	Arg
	290				295				300						
Ser	Leu	Arg	Leu	His	Arg	Phe	Thr	Arg	Gly	Ala	Leu	Cys	Val	Phe	
	305				310				315						

<210> 71
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R45 (hGR45)

<400> 71															
Met	Ala	Thr	Glu	Leu	Asp	Lys	Ile	Phe	Leu	Ile	Leu	Ala	Ile	Ala	Glu
1				5				10				15			
Phe	Ile	Ile	Ser	Met	Leu	Gly	Asn	Val	Phe	Ile	Gly	Leu	Val	Asn	Cys
				20				25				30			
Ser	Glu	Gly	Ile	Lys	Asn	Gln	Lys	Val	Phe	Ser	Ala	Asp	Phe	Ile	Leu
				35			40					45			
Thr	Cys	Leu	Ala	Ile	Ser	Thr	Ile	Gly	Gln	Leu	Leu	Val	Ile	Leu	Phe
	50				55				60						
Asp	Ser	Phe	Leu	Val	Gly	Leu	Ala	Ser	His	Leu	Tyr	Thr	Thr	Tyr	Arg
	65				70				75					80	
Leu	Gly	Lys	Thr	Val	Ile	Met	Leu	Trp	His	Met	Thr	Asn	His	Leu	Thr
				85			90					95			

Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
 100 105 110
 His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly
 115 120 125
 Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp
 130 135 140
 Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp
 145 150 155 160
 Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp
 165 170 175
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro
 180 185 190
 Phe Ser Leu Phe Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val
 195 200 205
 Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser
 210 215 220
 Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu
 225 230 235 240
 Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Trp Ile
 245 250 255
 Phe Phe Met Leu Trp Asn Asn Lys Cys Ile Lys Phe Val Met Leu Ala
 260 265 270
 Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285
 Ser Lys Leu Gln Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn
 290 295 300
 Tyr Thr Lys Thr Pro Asn Pro Leu Pro Leu
 305 310

<210> 72
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human T2R46 (hGR46)

<400> 72
 Met Ser Phe Leu His Ile Val Phe Ser Ile Leu Val Val Val Ala Phe
 1 5 10 15

Ile Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Ile Asn Phe Ile
 20 25 30

Ala Trp Val Lys Lys Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile Ala
 35 40 45

Asp Lys Gln Ser Pro Glu Leu Val Cys Ser Gly
50 55

<210> 73
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R47 (hGR47)

<220>
<221> MOD_RES
<222> (1)..(65)
<223> Xaa = any amino acid

<400> 73
Met Leu Asn Ala Leu Tyr Ser Ile Leu Ile Ile Ile Ile Asn Ile Xaa
1 5 10 15

Phe Leu Ile Gly Ile Leu Gly Asn Gly Phe Ile Thr Leu Val Asn Gly
20 25 30

Ile Asp Trp Val Lys Met Xaa Lys Arg Ser Ser Ile Leu Thr Ala Leu
35 40 45

Thr Ile Ser Arg Ile Cys Leu Ile Ser Val Ile Met Val Arg Trp Phe
50 55 60

Ile
65

<210> 74
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<223> human T2R48 (hGR48)

<400> 74
Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu His Trp Tyr Ser
1 5 10 15

Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val Ile Ile Phe Ile
20 25 30

Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile Trp Leu Ala Thr
35 40 45

Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
50 55 60

<210> 75
<211> 72
<212> PRT
<213> Homo sapiens

<220>

<223> human T2R49 (hGR49)

<400> 75

Thr Val Thr Met Leu Ala Asn Leu Val Pro Phe Thr Val Thr Leu Ile
1 5 10 15

Ser Phe Leu Leu Leu Val Cys Ser Leu Cys Lys His Leu Lys Lys Met
20 25 30

His Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile
35 40 45

Lys Val Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile Tyr
50 55 60

Phe Val Ser Val Ile Ile Ser Ser
65 70

<210> 76

<211> 299

<212> PRT

<213> Homo sapiens

<220>

<223> human T2R50 (hGR50)

<400> 76

Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Val Thr
1 5 10 15

Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20 25 30

Thr Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Val
35 40 45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
65 70 75 80

Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Thr Gly His Phe Ser Asn
85 90 95

Trp Pro Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110

Phe Ser Asn Leu Ile Phe Leu Arg Leu Lys Arg Arg Val Lys Ser Val
115 120 125

Ile Leu Val Val Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
130 135 140

Phe Val Val Asn Met Asn Gln Ile Val Trp Thr Lys Glu Tyr Glu Gly
145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Arg Arg Ala Met Tyr Leu Ser Asp
165 170 175

Thr	Thr	Val	Thr	Met	Leu	Ala	Asn	Leu	Val	Pro	Phe	Thr	Val	Thr	Leu
				180				185						190	
Ile	Ser	Phe	Leu	Leu	Leu	Val	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys
				195			200				205				
Met	Gln	Leu	His	Gly	Lys	Gly	Ser	Gln	Asp	Pro	Ser	Thr	Lys	Val	His
	210				215				220						
Ile	Lys	Val	Leu	Gln	Thr	Val	Ile	Ser	Phe	Phe	Leu	Leu	Cys	Ala	Ile
225			230			235			240						
Tyr	Phe	Val	Ser	Val	Ile	Ile	Ser	Val	Trp	Ser	Phe	Lys	Asn	Leu	Glu
	245					250				255					
Asn	Lys	Pro	Val	Phe	Met	Phe	Cys	Gln	Ala	Ile	Gly	Phe	Ser	Cys	Ser
	260					265				270					
Ser	Ala	His	Pro	Phe	Ile	Leu	Ile	Trp	Gly	Asn	Lys	Lys	Leu	Lys	Gln
	275					280				285					
Thr	Tyr	Leu	Ser	Val	Leu	Trp	Gln	Met	Arg	Tyr					
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<210> 77

<211> 335

<212> PRT

<213> Rattus sp.

<220>

<223> rat T2R01 (rGR01)

<400> 77

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Phe	Val	Thr	Gly	Val	Leu	Ala	Asn	Gly	Leu	Ile	Val	Val	Val	His	Ala
				20				25				30			

Ile	Asp	Leu	Ile	Met	Trp	Lys	Lys	Met	Ala	Pro	Leu	Asp	Leu	Leu	Leu
				35				40			45				

Phe	Cys	Leu	Ala	Thr	Ser	Arg	Ile	Ile	Leu	Gln	Leu	Cys	Ile	Leu	Phe
	50				55				60						

Ala	Gln	Leu	Cys	Leu	Phe	Ser	Leu	Val	Arg	His	Thr	Leu	Phe	Glu	Asp
	65				70				75			80			

Asn	Ile	Thr	Phe	Val	Phe	Ile	Ile	Asn	Glu	Leu	Ser	Leu	Trp	Phe	Ala
				85				90			95				

Thr	Trp	Leu	Gly	Val	Phe	Tyr	Cys	Ala	Lys	Ile	Ala	Thr	Ile	Pro	His
				100				105			110				

Pro	Leu	Phe	Leu	Trp	Leu	Lys	Met	Arg	Ile	Ser	Arg	Leu	Val	Pro	Trp
				115			120		125						

Leu	Ile	Leu	Gly	Ser	Val	Leu	Tyr	Val	Ile	Ile	Thr	Thr	Phe	Ile	His
				130			135		140						

Ser Arg Glu Thr Ser Ala Ile Leu Lys Pro Ile Phe Ile Ser Leu Phe
 145 150 155 160
 Pro Lys Asn Ala Thr Gln Val Gly Thr Gly His Ala Thr Leu Leu Ser
 165 170 175
 Val Leu Val Leu Gly Leu Thr Leu Pro Leu Phe Ile Phe Thr Val Ala
 180 185 190
 Val Leu Leu Leu Ile Tyr Ser Leu Trp Asn Tyr Ser Arg Gln Met Arg
 195 200 205
 Thr Met Val Gly Thr Arg Glu Tyr Ser Gly His Ala His Ile Ser Ala
 210 215 220
 Met Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Leu Ser His Tyr Met
 225 230 235 240
 Val Ala Val Leu Ile Ser Thr Gln Val Leu Tyr Leu Gly Ser Arg Thr
 245 250 255
 Phe Val Phe Cys Leu Leu Val Ile Gly Met Tyr Pro Ser Ile His Ser
 260 265 270
 Ile Val Leu Ile Leu Gly Asn Pro Lys Leu Lys Arg Asn Ala Lys Met
 275 280 285
 Phe Ile Val His Cys Lys Cys Cys His Cys Thr Arg Ala Trp Val Thr
 290 295 300
 Ser Arg Ser Pro Arg Leu Ser Asp Leu Pro Val Pro Pro Thr His Pro
 305 310 315 320
 Ser Ala Asn Lys Thr Ser Cys Ser Glu Ala Cys Ile Met Pro Ser
 325 330 335

<210> 78
 <211> 1331
 <212> DNA
 <213> Rattus sp.

<220>
 <223> rat T2R01 (rGR01)

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 gcagtttgc actggggct tggcaaattgg cctcattgtg gttgtccatg ctattgactt 180
 gatcatgtgg aagaaaatgg ccccgttgg tctgcttcta ttttgcctgg cgacttctcg 240
 gatcattctg cagttatgtt tattgttgc acaattgtgt ctattctctt tggtgagaca 300
 cactttattt gaggacaata ttacctttgt cttcatcata aatgaactga gtctttgggt 360
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 tctgtggctg aagatgagga tatccaggtt ggtaccatgg ctgatcctgg gatctgtgct 480
 ctatgttaattt attactactt tcatccatag cagagagact tcagcaatcc ttaaaaccaat 540
 ttttataagc cttttccata aaaatgcaac tcaagtcggg acagggcatg ccacactact 600
 ctcagtcctg gtccttggc tcacactgcc gttgttcattt tttactgttg ctgttctgct 660
 cttgatatac tccctgtgga attatagcag gcagatgagg actatggtag gcaccaggaa 720
 gtatagcggg catgctcaca tcagtgcattt gctgtccattt ctatcattcc tcatcctcta 780
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 aacctttgtt ttctgttttac tggtttattgg tatgtacccc tcaatacact cgattgtctt 900

aatttttagga aatccctaagc tgaaaacgaaa tgcaaaaaatg ttcattgtcc attgttaagtg 960
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 <211> 333
 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T2R02 (rGR02)

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 Ala Leu Val Asn Ile Met Asp Trp Leu Lys Arg Arg Arg Ile Ser Thr
 35 40 45
 Ala Asp Gln Ile Leu Thr Ala Leu Ala Leu Thr Arg Leu Ile Tyr Val
 50 55 60
 Trp Ser Val Leu Ile Cys Ile Leu Leu Leu Phe Leu Cys Pro His Leu
 65 70 75 80
 Ser Met Arg Pro Glu Met Phe Thr Ala Ile Gly Val Ile Trp Val Val
 85 90 95
 Asp Asn His Phe Ser Ile Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
 100 105 110
 Phe Leu Lys Ile Ala Ser Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
 115 120 125
 Trp Arg Val Lys Lys Val Val Leu Met Ile Ile Leu Ile Ser Leu Ile
 130 135 140
 Phe Leu Met Leu Asn Ile Ser Ser Leu Gly Met Tyr Asp His Phe Ser
 145 150 155 160
 Ile Asp Val Tyr Glu Gly Asn Met Ser Tyr Asn Leu Val Asp Ser Thr
 165 170 175
 His Phe Pro Arg Ile Phe Leu Phe Thr Asn Ser Ser Lys Val Phe Leu
 180 185 190
 Ile Ala Asn Ser Ser His Val Phe Leu Pro Ile Asn Ser Leu Phe Met
 195 200 205
 Leu Ile Pro Phe Thr Val Ser Leu Val Ala Phe Phe Val Leu Phe Leu
 210 215 220

Ser Leu Trp Lys His His Lys Lys Met Gln Val Asn Ala Lys Gly Pro
225 230 235 240

Arg Asp Ala Ser Thr Met Ala His Thr Lys Ala Leu Gln Ile Gly Phe
245 250 255

Ser Phe Leu Leu Leu Tyr Ala Ile Tyr Leu Leu Phe Ile Ile Thr Gly
260 265 270

Ile Leu Asn Leu Asp Leu Met Arg Cys Ile Val Ile Leu Leu Phe Asp
275 280 285

His Ile Ser Gly Ala Val Phe Ser Ile Ser His Ser Phe Val Leu Ile
290 295 300

Leu Gly Asn Ser Lys Leu Arg Gln Ala Thr Leu Ser Val Leu Pro Cys
305 310 315 320

Leu Arg Cys Arg Ser Lys Asp Met Asp Thr Val Val Phe
325 330

<210> 80

<211> 2438

<212> DNA

<213> Rattus sp.

<220>

<223> rat T2R02 (rGR02)

<400> 80

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atgagaattc attatttgat gcagttctg aaaactggat gtgaaatact ggtatgaagca 180
gaggtgatga ccccttgaa attaaaaaagc caagatgttc atggagaaat tataaaacaa 240
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 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T2R03 (rGR03)

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 35 40 45
 Leu Ile Ser Leu Gly Ile Ser His Phe Cys Leu Gln Trp Thr Ser Met
 50 55 60
 Leu Tyr Asn Phe Gly Thr Tyr Ser Arg Pro Val Leu Leu Phe Trp Lys
 65 70 75 80
 Val Ser Val Val Trp Glu Phe Met Asn Val Leu Thr Phe Trp Leu Thr
 85 90 95
 Ser Leu Leu Ala Val Leu Tyr Cys Val Lys Val Ser Ser Phe Ser His
 100 105 110
 Pro Val Phe Leu Trp Leu Arg Leu Lys Ile Leu Lys Leu Val Leu Trp
 115 120 125
 Leu Leu Leu Gly Ala Leu Ile Ala Ser Cys Leu Ser Ile Ile Pro Ser
 130 135 140
 Val Val Lys Tyr His Ile Gln Met Glu Leu Leu Thr Leu Asp His Leu
 145 150 155 160
 Pro Lys Asn Ser Ser Leu Ile Leu Arg Leu Gln Met Phe Glu Trp Tyr
 165 170 175
 Phe Ser Asn Pro Phe Lys Met Ile Gly Phe Gly Val Pro Phe Leu Val
 180 185 190
 Phe Leu Ile Ser Ile Ile Leu Leu Thr Val Ser Leu Val Gln His Trp
 195 200 205

Gly Gln Met Lys His Tyr Ser Ser Ser Ser Ser Ser Leu Arg Ala Gln
 210 215 220
 Cys Thr Val Leu Lys Ser Leu Ala Thr Phe Phe Ile Phe Phe Thr Ser
 225 230 235 240
 Tyr Phe Leu Thr Ile Val Val Ser Phe Ile Gly Thr Val Phe Asp Lys
 245 250 255
 Lys Ser Trp Phe Trp Val Cys Glu Ala Val Ile Tyr Gly Leu Val Cys
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 Ile His Phe Thr Ser Leu Met Met Ser Asn Pro Thr Leu Lys Lys Ala
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 Leu Arg Leu Gln Phe Trp Ser Pro Glu Ser Ser
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<210> 82
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 <212> DNA
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<220>
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 <223> n = g, a, c or t

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 aaaaaaaaaa aa 6552

<210> 83
 <211> 308
 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T2R04 (rGR04)

<400> 83
 Met Leu Ser Ala Ala Glu Gly Ile Leu Leu Cys Val Val Thr Ser Glu
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Ala Val Leu Gly Val Leu Gly Asp Thr Phe Ile Ala Leu Ala Asn Cys
 20 25 30

Met Glu Tyr Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Ile Leu
 35 40 45

Ile Gly Leu Ala Ile Ser Arg Ile Gly Val Val Trp Ile Ile Ile Leu
 50 55 60

Gln Gly Tyr Met Gln Val Phe Phe Pro His Ile Leu Thr Phe Gly Asn
 65 70 75 80

Ile Thr Glu Tyr Ile Thr Tyr Ile Trp Val Phe Leu Asn His Leu Ser
 85 90 95

Val Trp Phe Ala Thr Asn Leu Asn Ile Leu Tyr Phe Leu Lys Ile Ala
 100 105 110

Asn Phe Ser Asn Ser Val Phe Leu Trp Leu Lys Ser Arg Val Arg Val
 115 120 125

Val Phe Ile Phe Leu Ser Gly Cys Leu Leu Thr Ser Trp Leu Leu Cys
 130 135 140

Phe Pro Gln Phe Ser Lys Met Leu Asn Asn Ser Lys Met Tyr Trp Gly
 145 150 155 160

Asn Thr Ser Trp Leu Gln Gln Gln Lys Asn Val Phe Leu Ile Asn Gln
165 170 175

Ser Leu Thr Asn Leu Gly Ile Phe Phe Phe Ile Ile Val Ser Leu Ile
180 185 190

Thr Cys Phe Leu Leu Ile Val Phe Leu Trp Arg His Ile Arg Gln Met
195 200 205

His Ser Asp Gly Ser Gly Leu Arg Asp Leu Asn Thr Glu Ala His Val
210 215 220

Lys Ala Met Arg Val Leu Ile Ser Phe Ala Val Leu Phe Ile Leu His
225 230 235 240

Phe Val Gly Leu Ser Ile Gln Val Leu Cys Phe Phe Leu Pro Gln Asn
245 250 255

Asn Leu Leu Phe Ile Thr Gly Leu Ile Ala Thr Cys Leu Tyr Pro Cys
260 265 270

Gly His Ser Ile Ile Leu Ile Leu Gly Asn Lys Gln Leu Lys Gln Ala
275 280 285

Ser Leu Lys Ala Leu Gln His Leu Thr Cys Cys Glu Thr Lys Arg Asn
290 295 300

Leu Ser Val Thr
305

<210> 84
<211> 3449
<212> DNA
<213> Rattus sp.

<220>
<223> rat T2R04 (rGR04)

<400> 84
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tcacttaagt gtctggttt ctaccaacct caatatcctc tactttctaa agatagcaaa 480
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<210> 85

<211> 309

<212> PRT

<213> *Rattus* sp.

<220>

<223> rat T2R05 (rGR05)

<400> 85

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20 25 30

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35						40	.						45		

Thr Gly Leu Ala Ile Ser Arg Ile Cys Leu Val Trp Ile Leu Ile Thr
50 55 60

Glu Ala Tyr Ile Lys Ile Phe Ser Pro Gln Leu Leu Ser Pro Ile Asn
65 70 75 80

Ile Ile Glu Leu Ile Ser Tyr Leu Trp Ile Ile Thr Ser Gln Leu Asn
85 90 95

Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
100 105 110

Asn Phe Ser His His Ile Phe Leu Trp Leu Lys Arg Arg Ile Asn Ile
115 120 125

Val Phe Ala Phe Leu Ile Gly Cys Leu Leu Met Ser Trp Leu Phe Ser
130 135 140

Phe Pro Val Val Val Lys Met Val Lys Asp Lys Lys Met Leu Tyr Ile
145 150 155 160

Asn Ser Ser Trp Gln Ile His Met Lys Lys Ser Glu Leu Ile Ile Asn
165 170 175

Tyr Val Phe Thr Asn Gly Gly Val Phe Leu Leu Phe Ile Ile Met Leu
180 185 190

Ile Val Cys Phe Leu Leu Ile Ile Ser Leu Trp Arg His Ser Lys Trp
195 200 205

Met Gln Ser Asn Glu Ser Gly Phe Arg Asp Leu Asn Thr Glu Val His
210 215 220

Val Lys Thr Ile Lys Val Leu Leu Ser Phe Ile Ile Leu Phe Ile Leu
225 230 235 240

His Leu Ile Gly Ile Thr Ile Asn Val Ile Cys Leu Leu Val Pro Glu
245 250 255

Asn Asn Leu Leu Phe Val Phe Gly Leu Thr Ile Ala Phe Leu Tyr Pro
260 265 270

Cys Cys His Ser Leu Ile Leu Ile Leu Ala Asn Ser Arg Leu Lys Arg
275 280 285

Cys Phe Val Arg Ile Leu Gln Gln Leu Met Cys Ser Glu Glu Gly Lys
290 295 300

Glu Phe Arg Asn Thr
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<210> 86

<211> 1127

<212> DNA

<213> Rattus sp.

<220>

<223> rat T2R05 (rGR05)

<400> 86

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aagctatttt aaagatctgc gaagatgctg ggtgcaatgg aaggtgtcct cctttcagtt 180

gcaactagtg aggcttgct tggcattgta gggAACACAT tcattgcact tggactgc 240
 atggactgta ccaggaacaa gaatcttat aatattggct tcattctcac tggcttggca 300
 atttccagaa tctgcctcggt gttggatctta atcacagagg catacataaa aatattctct 360
 ccacagttgc tggctccat caacataatt gaactcatca gttatctatg gataattacc 420
 agtcaattga atggttgggt tgctaccagg ctcagttatct tttatttcctt caagatagca 480
 aattttccca accacatatt tctctggta aaaagaagaa ttaatataatgt tttgccttc 540
 ctgatagggt gcttacttat gtcatggcta tttctttcc cagtaggtgt gaagatgggt 600
 aaagataaaa aaatgctgta tataaactca tcttggcaaa tccacatgaa gaaaagttag 660
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 ggaagacaaa caatcagaaa tagtaagtga aaaaaaaaaa aaaaaaaaa 1127

<210> 87
 <211> 297
 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T2R06 (rGR06)

<400> 87
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 Phe Met Gly Trp Met Lys Asn Arg Lys Ile Thr Ala Ile Asp Leu Ile
 20 25 30
 Leu Ser Ser Leu Ala Met Ser Arg Ile Cys Leu Gln Cys Ile Ile Leu
 35 40 45
 Leu Asp Cys Ile Ile Leu Val Gln Tyr Pro Asp Thr Tyr Asn Arg Gly
 50 55 60
 Lys Glu Met Arg Ile Ile Asp Phe Phe Trp Thr Leu Thr Asn His Leu
 65 70 75 80
 Ser Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile
 85 90 95
 Ala Asn Phe Phe His Pro Leu Phe Leu Trp Ile Lys Trp Arg Ile Asp
 100 105 110
 Lys Leu Ile Leu Arg Thr Leu Leu Ala Cys Leu Ile Leu Ser Leu Cys
 115 120 125
 Phe Ser Leu Pro Val Thr Glu Asn Leu Ala Asp Asp Phe Arg Arg Cys
 130 135 140
 Val Lys Thr Lys Glu Arg Ile Asn Ser Thr Leu Arg Cys Lys Leu Asn
 145 150 155 160
 Lys Ala Gly Tyr Ala Ser Val Lys Val Asn Leu Asn Leu Val Met Leu
 165 170 175

Phe Pro Phe Ser Val Ser Leu Val Ser Phe Leu Leu Leu Ile Leu Ser
180 185 190

Leu Trp Arg His Thr Arg Gln Met Gln Leu Asn Val Thr Gly Tyr Asn
195 200 205

Asp Pro Ser Thr Thr Ala His Val Lys Ala Thr Lys Ala Val Ile Ser
210 215 220

Phe Leu Val Leu Phe Ile Val Tyr Cys Leu Ala Phe Leu Ile Ala Thr
225 230 235 240

Ser Ser Tyr Phe Met Pro Glu Ser Glu Leu Ala Val Ile Trp Gly Glu
245 250 255

Leu Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu
260 265 270

Gly Asn Ser Lys Leu Lys Gln Ala Ser Val Arg Val Leu Cys Arg Val
275 280 285

Lys Thr Met Leu Lys Gly Arg Lys Tyr
290 295

<210> 88

<211> 1304

<212> DNA

<213> Rattus sp.

<220>

<223> rat T2R06 (rGR06)

<400> 88

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<210> 89
<211> 305
<212> PRT
<213> Rattus sp.

<220>
<223> rat T2R07 (rGR07)

<400> 89
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Phe Ile Phe Gly Asn Val Thr Asn Gly Phe Ile Val Leu Thr Asn Cys
20 25 30
Ile Ala Trp Leu Ser Lys Arg Thr Leu Ser Phe Ile Gly Trp Ile Gln
35 40 45
Leu Phe Leu Ala Ile Ser Arg Val Val Leu Ile Trp Glu Met Leu Leu
50 55 60
Ala Trp Leu Lys Tyr Met Lys Tyr Ser Phe Ser Tyr Leu Ala Gly Thr
65 70 75 80
Glu Leu Arg Val Met Met Leu Thr Trp Val Val Ser Asn His Phe Ser
85 90 95
Leu Trp Leu Ala Thr Ile Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
100 105 110
Ser Phe Ser Arg Pro Val Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys
115 120 125
Val Leu Leu Leu Ile Leu Leu Gly Asn Leu Ile Phe Leu Met Phe Asn
130 135 140
Ile Leu Gln Ile Asn Thr His Ile Glu Asp Trp Met Asp Gln Tyr Lys
145 150 155 160
Arg Asn Ile Thr Trp Asp Ser Arg Val Asn Glu Phe Val Gly Phe Ser
165 170 175
Asn Leu Val Leu Leu Glu Met Ile Met Phe Ser Val Thr Pro Phe Thr
180 185 190
Val Ala Leu Val Ser Phe Ile Leu Ile Phe Ser Leu Trp Lys His
195 200 205
Leu Gln Lys Met His Leu Ser Ser Arg Gly Glu Arg Asp Pro Ser Thr
210 215 220
Lys Ala His Val Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu
225 230 235 240
Tyr Ala Thr Tyr Phe Ile Ser Phe Phe Ile Ser Leu Ile Pro Met Ala
245 250 255
His Lys Lys Gly Leu Asp Leu Met Phe Ser Leu Thr Val Gly Leu Phe
260 265 270

Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly His Ser Asn Leu
275 280 285

Arg His Ser Ser Cys Leu Val Ile Thr Tyr Leu Arg Cys Lys Glu Lys
290 295 300

Asp
305

<210> 90
<211> 3994
<212> DNA
<213> Rattus sp.

<220>
<223> rat T2R07 (rGR07)

<220>
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<223> n = g, a, c or t

<400> 90
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 atgtacttac aatatacataa agtttattga attccttta tcacttatgc agcctttct 2400
 tactattcta ttcttattcta ttcttattcta ttcttattcta ttcttattcta 2460
 ttcttattcta ttcttattcta gaatctaacc tatacattca ttctggcaa aacaacttat 2520
 atcatctcct taatttattt atcaatttaat ctaacatctt gaagtttattt aatctaata 2580
 taaggactt gtaaagtcac aaatttattt atacttcaca aaattcatta ttttatggaa 2640
 ctgcagcatt gcctgggcca ggagtcacaa gagttccaga gttgacttta ttggcatctg 2700
 cctggctaac tgaaggatca gtttctgtg tacaataatt ttgtgtatct ctttgatgc 2760
 aagatatgaa aaataatttc agtctaaag tggctttaaa ttgaaactc tctggccaga 2820
 atctaactat tgatgaccag tttgcacat ggactcagtg tcttcttattt cttttaaaata 2880
 agcaacatct tgaatgctt tcttgcgtat taggcaaata attaacaaca tgtttctatg 2940
 attgtctcaa taacaataact atatttctca cagttttaa tttttatggc aaagttggct 3000
 aataagaatt ttttcaaat tatcaaacgt gaagaaaact tgacattta tttcatggag 3060
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 acaaatgaca ttatatactt ggtgtgaca aataaggccc aaagaaatgt ttgaaaatca 3240
 tgatctcatt tctattctt ttatttaagt atagcataag caaaattctg atgggtgtct 3300
 tggcccatat ctttgaacac agtgttagtgg tgaagacttt tccaaatattt atgtcatatt 3360
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 atatagctat cctgaaatcc attaagttaga cctgactggc ttaaatctca cagaaattca 3660
 cctaccttt ccatgattgc taaaattaaa gacatgtgcc gacatattgg gcacattcag 3720
 accttttgc aactgtctt caactcattt ggacctactg agaagtattc aaaatattt 3780
 gttgtttaa ataaaaggaa agtgggtcta tattacttga attggataga gaaattttca 3840
 cttacaagtg atattgaaaa tgggggagaa ttttttag cataagcacc agaacacaaa 3900
 gcaattctt taaaacttt atcgataaaat tggataaaatg taaaaaaaaga aaaaataaaa 3960
 tatacgaact attatgaaaa aaaaaaaaaa aaaa 3994

<210> 91
 <211> 314
 <212> PRT
 <213> Rattus sp.

<220>
 <223> rat T2R08 (rGR08)

<400> 91
 Met Glu Pro Val Ile His Val Phe Ala Thr Leu Leu Ile His Val Glu
 1 5 10 15

Phe Ile Phe Gly Asn Leu Ser Asn Gly Leu Ile Val Leu Ser Asn Phe
 20 25 30

Trp Asp Trp Val Val Lys Arg Lys Leu Ser Thr Ile Asp Lys Ile Leu
 35 40 45

Leu Thr Leu Ala Ile Ser Arg Ile Thr Leu Ile Trp Glu Met Tyr Ala
 50 55 60

Cys Phe Lys Ile Val Tyr Gly Ser Ser Ser Phe Ile Phe Gly Met Lys
 65 70 75 80

Leu Gln Ile Leu Tyr Phe Ala Trp Ile Leu Ser Ser His Phe Ser Leu
 85 90 95

Trp Phe Ala Thr Ala Leu Ser Ile Phe Tyr Leu Leu Arg Ile Ala Asn
 100 105 110

Cys Ser Trp Lys Ile Phe Leu Tyr Leu Lys Trp Arg Leu Lys Gln Val
 115 120 125
 Ile Val Gly Met Leu Leu Ala Ser Leu Val Phe Leu Pro Gly Ile Leu
 130 135 140
 Met Gln Arg Thr Leu Glu Glu Arg Pro Tyr Gln Tyr Gly Gly Asn Thr
 145 150 155 160
 Ser Glu Asp Ser Met Glu Thr Asp Phe Ala Lys Phe Thr Glu Leu Ile
 165 170 175
 Leu Phe Asn Met Thr Ile Phe Ser Val Ile Pro Phe Ser Leu Ala Leu
 180 185 190
 Ile Ser Phe Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln Lys
 195 200 205
 Met Gln Leu Ser Ser Arg Gly His Gly Asp Pro Ser Thr Lys Ala His
 210 215 220
 Arg Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu Tyr Thr Ser
 225 230 235 240
 Tyr Phe Leu Ser Leu Leu Ile Ser Trp Ile Ala Gln Lys His His Ser
 245 250 255
 Lys Leu Val Asp Ile Ile Gly Ile Ile Thr Glu Leu Met Tyr Pro Ser
 260 265 270
 Val His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr
 275 280 285
 Ser Leu Trp Ile Leu Ser His Leu Lys Cys Arg Leu Lys Gly Glu Asn
 290 295 300
 Ile Leu Thr Pro Ser Gly Lys Pro Ile Asn
 305 310

<210> 92
 <211> 1886
 <212> DNA
 <213> Rattus sp.

<220>
 <223> rat T2R08 (rGR08)

<220>
 <221> modified_base
 <222> (1351)
 <223> n = g, a, c or t

<400> 92
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 ggaacctgtc attcacgtct ttgccactct actaatacat gtggagttca tttttggaa 120
 tctgagcaat ggattaatag tgggtcaaa cttctggac tgggtcgta aacgaaaact 180
 ttccacaatt gataaaattc ttcttacatt ggcaatttca agaatcactc tcatactgg 240
 aatgtatgct tggttaaaaa ttgtatatgg ttcatcttca tttatatttg ggatgaagt 300
 acaaattctt tattttgcct ggatccttc tagtcacttc agcctctggg ttgccacagc 360
 tctcagcatac ttttacttac tcagaatacg taactgctcc tggaaagatct tcctgtatct 420

gaaatggaga cttaaacaag tgattgtgg gatgttgctg gcaagcttgg ttttcttgcc 480
 tgaatcctg atgaaagga ctcttgaaga gaggccctat caatatggag gaaacacacaag 540
 tgaggattcc atggaaaactg actttgc当地 gtttacagag ctgattttt tcaacatgac 600
 tatattctct gtaataccat tttcattggc cttgatttct tttctctgc taatcttctc 660
 tttgtggaaa catctccaga agatgcagct cagttccaga ggacatggag accctagcac 720
 caaggcccac agaaatgc当地 tgagaattat ggttccctc ctcttgc当地 acacttcata 780
 tttcctgtct cttcttatat catggattgc tcagaagcat cacagtaaac tggttgc当地 840
 tattggattt attactgaac tcatgtatcc ttcagttccac tcatttatcc tgattctagg 900
 aaattctaaa ttaaagcaga cttctcttg gatactgagt catttgaat gtagactgaa 960
 aggagagaat attttaactc catctggca accaattaac tagctttat atattctgta 1020
 ttgcaaaaca atcagtgagt tagtggttca aggattccat ctttgactta ttgtatcatg 1080
 gaagtcatat agggagaggc tgaacaagct atcttctgta aattggcaag ggttgc当地 1140
 agtactggta ctgggacacc atccaaccat aaaaccttct aaccataacc tacctgactg 1200
 caagatatgc tgggacaatg gtggctcaga gattttggg ctggccaaacc aatgtctatt 1260
 ctttctttag gctcaactcaa taaggaggcc atgccc当地 ctgc当地 ggttgc当地 1320
 cagaatctct gatggsccaa tgatctatgg nagaacccag cattactggg aaaaaagaat 1380
 aatcactttt atgaatggtc aaatatttcc taaatatatt ctgatacact tgtacatcat 1440
 ttctcttcc caatcatcat cacagggact tctccccc当地 acctgatggg aacagatacc 1500
 aaaaatctaca gccaaataact aaatgcaggt tgggaaactc cacaaaagac tggaaaggaag 1560
 tactgtgaga gccagagtgg tccagaacac taggagaaca cagaacatcg aattaactaa 1620
 gcagcactca tagggttaat gtaaaataaa gcagcactca catagactgc acaggtgtac 1680
 tctagatcc ctgc当地 gttgtgggg tcaaacttgg gagtttggg ggactaataa 1740
 caatgtgaat aagtaagtct ctgacactta ttccc当地 tggaccctt ttccacattt 1800
 tgtattgtct taccacctt atatgaaggt ttctgaatag tccaaaaaaaaaaaaaaa 1860
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1886

<210> 93

<211> 309

<212> PRT

<213> Rattus sp.

<220>

<223> rat T2R09 (rGR09)

<400> 93

Met Leu Ser Ala Ala Glu Gly Ile Leu Leu Ser Ile Ala Thr Val Glu
 1 5 10 15

Ala Gly Leu Gly Val Leu Gly Asn Thr Phe Ile Ala Leu Val Asn Cys
 20 25 30

Met Asp Trp Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Leu Leu
 35 40 45

Phe Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Ile Leu Ile Leu
 50 55 60

Asp Ala Tyr Ala Lys Leu Phe Phe Pro Gly Lys Tyr Leu Ser Lys Ser
 65 70 75 80

Leu Thr Glu Ile Ile Ser Cys Ile Trp Met Thr Val Asn His Met Thr
 85 90 95

Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
 100 105 110

Asn Phe Ser His Tyr Ile Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys
 115 120 125

Val Phe Ala Phe Leu Leu Trp Cys Leu Leu Ile Ser Trp Ala Ile Ser
 130 135 140

 Phe Ser Phe Thr Val Lys Val Met Lys Ser Asn Pro Lys Asn His Gly
 145 150 155 160

 Asn Arg Thr Ser Gly Thr His Trp Glu Lys Arg Glu Phe Thr Ser Asn
 165 170 175

 Tyr Val Leu Ile Asn Ile Gly Val Ile Ser Leu Leu Ile Met Thr Leu
 180 185 190

 Thr Ala Cys Phe Leu Leu Ile Ile Ser Leu Trp Lys His Ser Arg Gln
 195 200 205

 Met Gln Ser Asn Val Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His
 210 215 220

 Val Lys Ala Ile Lys Phe Leu Ile Ser Phe Ile Ile Leu Phe Ile Leu
 225 230 235 240

 Tyr Phe Ile Gly Val Ala Val Glu Ile Ile Cys Met Phe Ile Pro Glu
 245 250 255

 Asn Lys Leu Leu Phe Ile Phe Gly Leu Thr Thr Ala Ser Val Tyr Pro
 260 265 270

 Cys Cys His Ser Val Ile Leu Ile Leu Thr Asn Ser Gln Leu Lys Gln
 275 280 285

 Ala Phe Val Lys Val Leu Glu Gly Leu Lys Phe Ser Glu Asn Gly Lys
 290 295 300

 Asp Leu Arg Ala Thr
 305

<210> 94
 <211> 2596
 <212> DNA
 <213> Rattus sp.

<220>
 <223> rat T2R09 (rGR09)

<400> 94
 ggacactgca gcagatctgc tatagaataa cagatacaaa catagcaacc tgcagagatg 60
 ctcagtgcag cagaaggcat ccttcttcc attgcaactg ttgaagctgg gctgggagtt 120
 ttagggaca catttatcgc cctggtaac tgcattggatt gggccaagaa caagaagctc 180
 tctaagatttgc ttcccttct ctttggctt gcaacttcca gaattttat tttatggata 240
 ttaattttag acgcatatgc aaagctattc tttccgggaa agtatttgc taagagtctg 300
 actgaaatca tctctgtat atggatgact gtgaatcaca tgactgtctg gttgccacc 360
 agcctcagca tcttcttattt cctaaaaata gcaaattttt cccactatat atttctctgg 420
 ttaaagagga gaactgataa agtatttgcc tttcttctgt ggtgtttattt aatttcatgg 480
 gcaatctccct tctcattcac tgtgaaagtg atgaagagca atccaaagaa tcatggaaac 540
 aggaccatgt ggacacattg ggagaagaga gaattcaca gtaactatgt ttaatcaat 600
 atggagtc tttctcttattt gatcatgacc ttaactgcat gtttcttgcattt aatttatttca 660
 ctggaaac acagcaggca gatgcagtct aatgtttcag gattcagaga tctcaacact 720
 gaagctcatg tgaaagccat aaaatttttta atttcatttca tcatcctttt catcttgcatt 780
 ttatagtg ttgcagtaga aatcatctgc atgtttatcc cagaaaacaa actgctattt 840
 attttgggt tgacaactgca atccgtctat ccctgctgc actcagtcat tctaatttca 900

<210> 95
<211> 137
<212> PRT
<213> *Rattus* sp.

<220>
<223> rat T2R10 (rGR10)

<400> 95
Met Phe Leu His Thr Ile Lys Gln Arg Asp Ile Phe Thr Leu Ile Ile
1 5 10 15

Ile Phe Phe Val Glu Ile Thr Met Gly Ile Leu Gly Asn Gly Phe Ile
20 25 30

Ala Leu Val Asn Ile Val Asp Trp Ile Lys Arg Arg Arg Ile Ser Ser
35 40 45

Val Asp Lys Ile Leu Thr Thr Leu Ala Leu Thr Arg Leu Ile Tyr Ala
50 55 60

Trp Ser Met Leu Ile Phe Ile Leu Leu Phe Ile Leu Gly Pro His Leu
 65 70 75 80

Ile Met Arg Ser Glu Ile Leu Thr Ser Met Gly Val Ile Trp Val Val
85 90 95

Asn Asn His Phe Ser Ile Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
 100 105 110

Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
115 120 125

Trp Arg Val Lys Lys Val Val Leu Met
130 135

<210> 96
<211> 818
<212> DNA
<213> Rattus sp.

<220>
<223> rat T2R10 (rGR10)

<400> 96
cccgccgtgc aggattcgcc acgagaatga aaactttgc tctactatgg tgcgtttctg 60
tgataccaca gaccataaaa caatcgagcc aaggatcaa gagctgaaac ttcatggaaagt 120
ggaaatcaaa ttcccttcct gataggtag cttatggaa ttcatggatct tattcaactt 180
cagaaaattt gatataagat acatgtctg gatgaagccg aattgtatctt tttggggaga 240
aaaaacgcca acatttataa taagggttta tgagacagtt cctggaaat ttggatattt 300
ccatgttagt aatgtgtaaa tgggatttttta aaacatgatt atttgttattt ttaacaacc 360
aacatgagga gctttttaaa tgccacttag acattataaa ctgaagcatg ttcttacaca 420
caataaaagca acgtgatatt ttacttttga taatcatatt ttttggaa ataacaatgg 480
gaatcttagg aaatggattt atagcactag tgaacattgt ggactggatc aagagaagaa 540
ggatttcttc agtggataag attctacta ccttggccct taccagactc atttatgcgt 600
ggctctatgtc cattttata ttgttattca tactggggccc gcatttgatt atgagatcag 660
aaatacttac atcaatgggt gttatctggg tggtaaccaa tcacttcagc atctggcttg 720
ctacatgcct cgggtcttt tattttctca agatagccaa ttttcttaac tctttgtttc 780
tttacctaaa gtggagagtt aaaaaagtg 818

<210> 97
<211> 105
<212> PRT
<213> Rattus sp.

<220>
<223> rat T2R11 (rGR11)

<220>
<221> MOD_RES
<222> (101)
<223> Xaa = any amino acid

<400> 97
Gly Ser Gly Asn Gly Phe Ile Val Ser Val Asn Gly Ser His Trp Phe
1 5 10 15

Lys Ser Lys Lys Ile Ser Leu Ser Asp Phe Ile Ile Thr Ser Leu Ala
20 25 30

Leu Phe Arg Ile Phe Leu Leu Trp Ile Ile Phe Thr Asp Ser Leu Ile
35 40 45

Ile Val Phe Ser Tyr His Ala His Asp Ser Gly Ile Arg Met Gln Leu
50 55 60

Ile Asp Val Phe Trp Thr Phe Thr Thr His Phe Ser Ile Trp Leu Ile
65 70 75 80

Ser Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile Ala Thr Phe Ser His
85 90 95

Pro Ser Phe Leu Xaa Leu Lys Ser Arg
100 105

<210> 98
<211> 315
<212> DNA
<213> Rattus sp.

<220>
<223> rat T2R11 (rGR11)

<400> 98
ggatccggaa acgggtttat cgtgtcagtc aatggcagcc attggttcaa gagcaagaag 60
atttctttgt ctgacttcat cattaccagc ttggccctct tcaggatctt tctgctgtgg 120
atcatcttta ctgatagcct cataatagtg ttctcttacc acgcccacga ctcagggata 180
aggatgcaac ttattgtatgt tttctggaca tttacaaccc acttcagttat ttggcttatac 240
tcctgtctca gtgtttctca ctgcctgaaa atagccactt tctcccaccc ctcattcctg 300
tagctcaaat ctaga 315

<210> 99
<211> 308
<212> PRT
<213> Rattus sp.

<220>
<223> rat T2R12 (rGR12)

<400> 99
Met Leu Ser Thr Val Ser Val Phe Phe Met Ser Ile Phe Val Leu Leu
1 5 10 15

Cys Phe Leu Gly Ile Leu Ala Asn Gly Phe Ile Val Leu Met Leu Ser
20 25 30

Arg Glu Trp Leu Trp Arg Gly Arg Leu Leu Pro Ser Asp Met Ile Leu
35 40 45

Leu Ser Leu Gly Thr Ser Arg Phe Cys Gln Gln Cys Val Gly Leu Val
50 55 60

Asn Ser Phe Tyr Tyr Ser Leu His Leu Val Glu Tyr Ser Arg Ser Leu
65 70 75 80

Ala Arg Gln Leu Ile Ser Leu His Met Asp Phe Leu Asn Ser Ala Thr
85 90 95

Phe Trp Phe Gly Thr Trp Leu Ser Val Leu Phe Cys Ile Lys Ile Ala
100 105 110

Asn Phe Ser His Pro Ala Phe Leu Trp Leu Lys Trp Arg Phe Pro Ala
115 120 125

Leu Val Pro Trp Leu Leu Leu Gly Ser Ile Leu Val Ser Phe Ile Val
130 135 140

Thr Leu Met Phe Phe Trp Gly Asn His Thr Val Tyr Gln Ala Phe Leu
 145 150 155 160
 Arg Arg Lys Phe Ser Gly Asn Thr Thr Phe Lys Glu Trp Asn Arg Arg
 165 170 175
 Leu Glu Ile Asp Tyr Phe Met Pro Leu Lys Leu Val Thr Thr Ser Ile
 180 185 190
 Pro Cys Ser Leu Phe Leu Val Ser Ile Leu Leu Ile Asn Ser Leu
 195 200 205
 Arg Arg His Ser Gln Arg Met Gln His Asn Ala His Ser Leu Gln Asp
 210 215 220
 Pro Asn Thr Gln Ala His Ser Arg Ala Leu Lys Ser Leu Ile Ser Phe
 225 230 235 240
 Leu Val Leu Tyr Ala Leu Ser Tyr Val Ser Met Val Ile Asp Ala Thr
 245 250 255
 Val Val Ile Ser Ser Asp Asn Val Trp Tyr Trp Pro Trp Gln Ile Ile
 260 265 270
 Leu Tyr Leu Cys Met Ser Val His Pro Phe Ile Leu Ile Thr Asn Asn
 275 280 285
 Leu Lys Phe Arg Gly Thr Phe Arg Gln Leu Leu Leu Ala Arg Gly
 290 295 300
 Phe Trp Val Thr
 305

<210> 100
 <211> 1295
 <212> DNA
 <213> Rattus sp.

 <220>
 <223> rat T2R12 (rGR12)

<400> 100
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 caggaggggc tgaaaatgcta tcaactgtat cagtttctt catgtcgatc tttgttctgc 120
 tctgttccct gggaaatcctg gcaaacgct tcattgtgct gatgctgagc agggaatggc 180
 tatggcgccg taggctgctc ccctcagaca tgatcctct cagtttggc acctcccgat 240
 tctgccagca gtgcgttggg ctggtaaca gtttctacta ttccctccac cttgttgagt 300
 actccaggag ctttgcctgt caactcatca gtctcacat ggacttcttg aactcagcca 360
 ctttctgggt tggcacctgg ctcagcgtcc tttctgtat caagattgct aacttctccc 420
 atcctgcctt cctgtgggtt aagtggagat tcccagcatt ggtgccttgg ctcctactgg 480
 gctctatctt ggtgtccttc atcgtaactc tgatgttctt ttggggaaac cacactgtct 540
 atcaggcatt cttaaggaga aagtttctg ggaacacaac ctttaaggag tggAACAGAA 600
 ggctggaaat agactatttc atgcctctga aacttgcac cacgtcaatt ccttgccttc 660
 tttttctagt ctcaattttg ctgttgatca attctctcag aaggcattca caaagaatgc 720
 agcacaatgc tcacagctt ccaagaccca acacccaggc tcacagcaga gccctgaagt 780
 cactcatctc atttctgggtt ctttacgcgc tgccttatgt gtccatggtc attgacgcta 840
 cagttgtcat ctcctcagat aacgtgtggt attggccctg gcaaattata ctttacttgc 900
 gcatgtccgt acatccattt atccttataca ctaataatct caagttccga ggcacccatca 960
 ggcagctact cctgtggcc agggattct gggtgaccta gaaggttgg tctcttatac 1020
 tgcaccctt gaagagactt aggtgagggt gacttccctt ggaagtgtatc tcatctacat 1080

gaaaaatgtct ttgttaggctg acatggggtc atactatgtg gttcctcctt gggaaagagg 1140
agaagaaaat acagggattc tgagcggtct tccttatctt gggatattat gaaaatggac 1200
attctgaatc ctgaaccagt attgatctga agtgc当地 acaatatgcc tgttcccttc 1260
atgtctgcta tcctcttggt acttattaaat tccct 1295

<210> 101
<211> 332
<212> PRT
<213> Rattus sp.

<220>
<223> rat T2R13 (rGR13)

<400> 101
Met Cys Gly Phe Pro Leu Ser Ile Gln Leu Leu Thr Gly Leu Val Gln
1 5 10 15

Met Tyr Val Ile Leu Ile Ile Ala Val Phe Thr Pro Gly Met Leu Gly
20 25 30

Asn Val Phe Ile Gly Leu Val Asn Tyr Ser Asp Trp Val Lys Asn Lys
35 40 45

Lys Ile Thr Phe Ile Asn Phe Ile Leu Ile Cys Leu Ala Ala Ser Arg
50 55 60

Ile Ser Ser Val Leu Val Val Phe Ile Asp Ala Ile Ile Leu Glu Leu
65 70 75 80

Thr Pro His Val Tyr His Ser Tyr Ser Arg Val Lys Cys Ser Asp Ile
85 90 95

Phe Trp Val Ile Thr Asp Gln Leu Ser Thr Trp Leu Ala Thr Cys Leu
100 105 110

Ser Ile Phe Tyr Leu Leu Lys Ile Ala His Phe Ser His Pro Leu Phe
115 120 125

Leu Trp Leu Lys Trp Arg Leu Arg Gly Val Leu Val Gly Phe Leu Leu
130 135 140

Phe Ser Leu Phe Ser Leu Ile Val Tyr Phe Leu Leu Glu Leu Leu
145 150 155 160

Ser Ile Trp Gly Asp Ile Tyr Val Ile Pro Lys Ser Asn Leu Thr Leu
165 170 175

Tyr Ser Glu Thr Ile Lys Thr Leu Ala Phe Gln Lys Ile Ile Val Phe
180 185 190

Asp Met Leu Tyr Leu Val Pro Phe Leu Val Ser Leu Ala Ser Leu Leu
195 200 205

Leu Leu Phe Leu Ser Leu Val Lys His Ser Gln Asn Leu Asp Arg Ile
210 215 220

Ser Thr Thr Ser Glu Asp Ser Arg Ala Lys Ile His Lys Lys Ala Met
225 230 235 240

Lys Met Leu Leu Ser Phe Leu Val Leu Phe Ile Ile His Ile Phe Cys
245 250 255

Met Gln Leu Ser Arg Trp Leu Phe Phe Leu Phe Pro Asn Asn Arg Ser
260 265 270

Thr Asn Phe Leu Leu Leu Thr Leu Asn Ile Phe Pro Leu Ser His Thr
275 280 285

Phe Ile Ile Ile Leu Gly Asn Ser Lys Leu Arg Gln Arg Ala Met Arg
290 295 300

Val Leu Gln His Leu Lys Ser Gln Leu Gln Glu Leu Ile Leu Ser Leu
305 310 315 320

His Arg Leu Ser Arg Val Phe Thr Met Glu Ile Ala
325 330

<210> 102

<211> 1287

<212> DNA

<213> Rattus sp.

<220>

<223> rat T2R13 (rGR13)

<400> 102

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gcaagataac tatgggaaag gatgatttc ggtggatgtt tgagaactga gcagcaaggc 180
aaattgtatg atgtgtggat tccctcttc tattcaactg cttactggat tggttcaa 240
gtacgtgata ttgataatag cagtgtttac acctggaatg ctgggaaatg tgttcattgg 300
actggtaaac tactctgact gggtaaaaaa caagaaaaatc accttcatca acttcatcct 360
gatctgtttg gcagcgtcca gaatcagtc tgtgttggtg gtatttattg atgcaatcat 420
cctagaacta actcctcatg tctatcatc ttacagtcga gtgaaatgct ctgatata 480
ctgggttata actgaccagc tgtcaacgtg gctgccacc tgcctcagca ttttctactt 540
actcaaaata gcccacttct cccatccct tttcccttgg ttgaagtgg aattgagagg 600
agtgcgtgtt ggtttcttc tattttctt gttctcattt attgtttatt ttctactcct 660
ggaattactg tctatttggg gagatatta tgtatccct aaaagcaatc tgactttata 720
ttcagaaaca attaagaccc ttgctttca aaagataatt gttttgata tgctatattt 780
agtcccattt cttgtgtccc tagcctcatt gctcccttta tttttatcct tggtaagca 840
ctcccaaaac cttgacagga tttctaccac ctctgaagat tccagagcca agatccacaa 900
gaaggccatg aaaatgctat tatctttctt cgtctcttt ataattcaca tttttgcat 960
gcagttgtca cggtggttat tcttttggtt tccaaacaac aggtcaacta attttcttt 1020
gttaacattt aacatcttcc cattatctca tacattcatt atcatcctgg gaaacagcaa 1080
gttgcacaa agagcaatga gggctctgca acatcttaaa agccaaacttc aagagttgat 1140
cctctccctt catagattgt ccagagtctt cactatggaa atagcttaaa ggggagactt 1200
ggaaggtcac tggtaacttg ttctccgct gagttctgtt aagtaatgct ggacatata 1260
gaactatccc tagtgcatac tgatatt 1287

<210> 103

<211> 68

<212> PRT

<213> Rattus sp.

<220>

<223> rat T2R14 (rGR14)

<400> 103
Val Ala Asn Ile Met Asp Trp Val Lys Arg Arg Lys Leu Ser Ala Val
1 5 10 15

Asp Gln Leu Leu Thr Val Leu Ala Ile Ser Arg Ile Thr Leu Leu Trp
20 25 30

Ser Leu Tyr Ile Leu Lys Ser Thr Phe Ser Met Val Pro Asn Phe Glu
35 40 45

Val Ala Ile Pro Ser Thr Arg Leu Thr Asn Leu Val Trp Ile Ile Ser
50 55 60

Asn His Phe Asn
65

<210> 104

<211> 206

<212> DNA

<213> Rattus sp.

<220>

<223> rat T2R14 (rGR14)

<400> 104

ctgtggcaaa cataatggat tgggtcaaga gaaggaagct ctctgcagtg gatcagctcc 60
tcactgtgct ggccatctcc agaatcactc tgggtggtc attgtacata ctgaaatcaa 120
cattttcaat ggtgccaaac tttgaggtag ctataccgtc aacaagacta actaatctg 180
tctggataat ttctaaaccat tttaat 206

<210> 105

<211> 327

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R01 (mGR01)

<400> 105

Met Gln His Leu Leu Lys Thr Ile Phe Val Ile Cys His Ser Thr Leu
1 5 10 15

Ala Ile Ile Leu Ile Phe Glu Leu Ile Ile Gly Ile Leu Gly Asn Gly
20 25 30

Phe Met Ala Leu Val His Cys Met Asp Trp Val Lys Arg Lys Lys Met
35 40 45

Ser Leu Val Asn Lys Ile Leu Thr Ala Leu Ala Ile Ser Arg Ile Phe
50 55 60

His Leu Ser Leu Leu Leu Ile Ser Leu Val Ile Phe Phe Ser Tyr Ser
65 70 75 80

Asp Ile Pro Met Thr Ser Arg Met Thr Gln Val Ser Asn Asn Val Trp
85 90 95

Ile Ile Val Asn His Phe Ser Ile Trp Leu Ser Thr Cys Leu Ser Val
100 105 110

Leu Tyr Phe Leu Lys Ile Ser Asn Phe Ser Asn Ser Phe Phe Leu Tyr
 115 120 125
 Leu Lys Trp Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser
 130 135 140
 Leu Leu Leu Ile Leu Asn Ile Leu Leu Ile Asn Leu Glu Ile Ser
 145 150 155 160
 Ile Cys Ile Lys Glu Cys Gln Arg Asn Ile Ser Cys Ser Phe Ser Ser
 165 170 175
 His Tyr Tyr Ala Lys Cys His Arg Gln Val Ile Arg Leu His Ile Ile
 180 185 190
 Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu Leu
 195 200 205
 Ile Phe Ser Leu Trp Thr Leu His Gln Arg Met Gln Gln His Val Gln
 210 215 220
 Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln Thr
 225 230 235 240
 Val Ile Ala Phe Phe Leu Leu Tyr Ser Ile Phe Ile Leu Ser Val Leu
 245 250 255
 Ile Gln Asn Glu Leu Leu Lys Lys Asn Leu Phe Val Val Phe Cys Glu
 260 265 270
 Val Val Tyr Ile Ala Phe Pro Thr Phe His Ser Tyr Ile Leu Ile Val
 275 280 285
 Gly Asp Met Lys Leu Arg Gln Ala Cys Leu Pro Leu Cys Ile Ile Ala
 290 295 300
 Ala Glu Ile Gln Thr Thr Leu Cys Arg Asn Phe Arg Ser Leu Lys Tyr
 305 310 315 320
 Phe Arg Leu Cys Cys Ile Phe
 325

<210> 106
 <211> 1374
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R01 (mGR01)

<400> 106
 agctgtgcgt gagcaaagca tttcttgcgt gccacttctg agctgtgtga ggagacacat 60
 tatcacggaa agagattcag actctgtcgc tgcataaacct gtatgtttgc tcctctttta 120
 ctgtgaaggc agagttacga aaaaaaatgt tatgagaacc aactcagaaa ttgacaaaaaa 180
 ttttctaaat gtcattttta aaaattatat ttccaaatggaa aatgtgagca aatctttata 240
 actaatatat aaaatgcgc atctttaaa gacaatattt gttatctgcc atagcacact 300
 tgcaatcatt ttaatctttg aattaataat tggatttta gggaaatgggt tcatggccct 360
 ggtgcactgt atggactggg ttaagagaaa gaaaatgtcc ttatgttata aaatcctcac 420
 tgcttggca atctccagaa tttttcatct cagtttattt cttataagtt tagtcatatt 480
 cttttcatat tctgatattc ctatgacttc aaggatgaca caagttagtca ataatgtttg 540

gattatagtc	aatcatttca	gtatctggct	ttctacatgc	ctcagtgtcc	tttattttct	600
caagatatcc	aatttttcta	actcttttt	tctttatcta	aagtggagag	ttgaaaaagt	660
agtttcagtt	acactgttg	tgtcattgt	cctcctgatt	ttaaatattt	tattaattaa	720
cttggaaatt	agcatatgc	taaagaatg	tcaaagaaac	atatcatgca	gcttcagttc	780
tcattactat	gcaaagtgtc	acaggcagg	gataaggc	cacattattt	tcctgtctgt	840
ccccgttgtt	ttgtccctgt	caactttct	cctgctc	ttctccctgt	ggacacttca	900
ccagaggatg	cagcagcatg	ttcagggagg	cagagatg	ccacttcaa	cccacttcaa	960
agccctacaa	actgtgattt	cattttct	actatatttcc	attttattt	tgtctgtt	1020
aatacaaata	tgaattactg	aagaaaaatc	tttcgtt	attttgtgag	gttgtatata	1080
tagctttcc	gacattccat	tcata	tattgt	agacatgaag	ctgagacagg	1140
cctgcctgcc	tctctgtatt	atcgcagct	aaattcagac	tacactatgt	agaaatttta	1200
gatcaactaaa	gtactttaga	ttatgtt	taattctagac	aaaaattaac	tgatacaat	1260
gtctttgtt	ttttcattt	taaatac	ttaatttga	ctgcatgaaa	ttgatttctg	1320
cttgcattt	tcactgatta	aaactattaa	taattttaact	agttgtatac	aagg	1374

<210> 107
<211> 327
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R02 (mGR02)

<400> 107
Met Glu Ser Val Leu His Asn Phe Ala Thr Val Leu Ile Tyr Val Glu
1 5 10 15

Phe Ile Phe Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ser Asn Phe
 20 25 30

Leu Asp Trp Val Ile Lys Gln Lys Leu Ser Leu Ile Asp Lys Ile Leu
35 40 45

Leu Thr Leu Ala Ile Ser Arg Ile Thr Leu Ile Trp Glu Ile Tyr Ala
50 55 60

Trp Phe Lys Ser Leu Tyr Asp Pro Ser Ser Phe Leu Ile Gly Ile Glu
 65 70 75 80

Trp Leu Ala Thr Thr Leu Ser Val Phe Tyr Leu Leu Arg Ile Ala Asn
 100 105 110

Cys Ser Trp Gln Ile Phe Leu Tyr Leu Lys Trp Arg Leu Lys Gln Leu
 115 120 125

Ile Val Gly Met Leu Leu Gly Ser Leu Val Phe Leu Leu Gly Asn Leu
 130 135 140

Met Gln Ser Met Leu Glu Glu Arg Phe Tyr Gln Tyr Gly Arg Asn Thr
 145 150 155 160

Ser Val Asn Thr Met Ser Asn Asp Leu Ala Met Trp Thr Glu Leu Ile
 165 170 175

Phe Phe Asn Met Ala Met Phe Ser Val Ile Pro Phe Thr Leu Ala Leu
 180 185 190

Ile	Ser	Phe	Leu	Leu	Leu	Ile	Phe	Ser	Leu	Trp	Lys	His	Leu	Gln	Lys
195						200					205				
Met	Gln	Leu	Ile	Ser	Arg	Arg	His	Arg	Asp	Pro	Ser	Thr	Lys	Ala	His
210						215					220				
Met	Asn	Ala	Leu	Arg	Ile	Met	Val	Ser	Phe	Leu	Leu	Tyr	Thr	Met	
225						230					235			240	
His	Phe	Leu	Ser	Leu	Leu	Ile	Ser	Trp	Ile	Ala	Gln	Lys	His	Gln	Ser
	245						250					255			
Glu	Leu	Ala	Asp	Ile	Ile	Gly	Met	Ile	Thr	Glu	Leu	Met	Tyr	Pro	Ser
	260						265					270			
Val	His	Ser	Cys	Ile	Leu	Ile	Leu	Gly	Asn	Ser	Lys	Leu	Lys	Gln	Thr
	275						280					285			
Ser	Leu	Cys	Met	Leu	Arg	His	Leu	Arg	Cys	Arg	Leu	Lys	Gly	Glu	Asn
	290						295					300			
Ile	Thr	Ile	Ala	Tyr	Ser	Asn	Gln	Ile	Thr	Ser	Phe	Cys	Val	Phe	Cys
305											315			320	
Val	Ala	Asn	Lys	Ser	Met	Arg									
						325									

<210> 108
 <211> 1759
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R02 (mGR02)

<400> 108
 cagcacagtg aaaaactcat gggccacttg gtcacccagg gacaggcgac gctgttatat 60
 gccaagcttt ctatgaacat ggaatctgtc cttcacaact ttgccactgt actaatatac 120
 gtggagttta ttttggaa tttagcaat ggattcatag tgggtcaaa cttcttggac 180
 tgggtcatta aacaaaagct ttccctaata gataaaaattc ttcttacatt ggcaatttca 240
 agaatcactc tcacatggaa aatatatgct tggttaaaaa gtttatatga tccatcttcc 300
 ttttaattt gaatagaatt tcaaattatt tatttttagct gggcccttcc tagtcaactc 360
 agcctctggc ttgcacaac tctcagcgtc ttttatttac tcagaatagc taactgctcc 420
 tggcagatct ttcttctattt gaaatggaga cttaaacaac tgattgtggg gatgttgctg 480
 ggaagcttg. tgttttgtc tggaaatctg atgaaagca tgcttgaaga gaggttctat 540
 caaatggaa ggaacacaag tggaaatacc atgagcaatg accttgcattt gttggaccgag 600
 ctgatcttt tcaacatggc tatgttctct gtaataccat ttacatttgc cttgatttct 660
 tttctctgc taattttctc ttgtggaaa catctccaga agatgcagct catttccaga 720
 agacacagag acccttagcac caaggccac atgaatgcct tgagaattat ggtgtccttc 780
 ctcttgcctt ataccatgca ttccctgtct cttcttataat catggattgc tcaaaaagcat 840
 cagagtgaac tggctgatat tattggatg ataaactgaac tcatgtatcc ttcaagtccat 900
 tcatgtatcc tgattctagg aaattctaaa ttaaagcaga cttctcttg tatgctgagg 960
 catttggat gtggctgaa aggagagaat atcacaattt catatagcaa ccaaataact 1020
 agcttttgc tattctgtgt tgcaaaacaaa tctatgaggt agttgttcaa ggaatccttc 1080
 cttgacttat tggatcatgg aagtcatatg ggggagctg aaagagctgt cttctgtaa 1140
 caagggttgc atacactatg ggggctggaa caccacccaa agcacaac ctagctataa 1200
 cctatcctgg ctgcaggata tgctggaaaca atggctggctt gggaaattgtg ggactggcaa 1260
 agcaatagct agtctaactt gaggcccatt ccacacggagg aagctcatgc ccacctctgc 1320
 ctggatggcc aggaagcaaa atcttgcattt ccccaagacc tatggtaaac tgaacactac 1380
 tggaaaaaga aagactctgtt ttaatgcattt tcctaataatattt attctgtataa 1440

actcatatat tagtccctgt cctaattatc atcaactggg ctccttccca gcacctgatg 1500
 ggaggcagata gagatctaca tccaaatagt aagtgtatct tggggaaactc cacttaagaa 1560
 tagaaggaaac aattatgaga gccagagtga tccagaacac taggatcaca gaatcaacta 1620
 agcagcatgc ataggggtta atggagactg aagtggcaat cacagagcct gcataggct 1680
 acactaagtgc ctctgtgtat atactgtggc tgtagctt aggaatttg ttggactcct 1740
 aacaatggat aaggaattc 1759

<210> 109
 <211> 312
 <212> PRT
 <213> Mus sp.

<220>
 <223> mouse T2R03 (mGR03)

<400> 109
 Met Val Leu Thr Ile Arg Ala Ile Leu Trp Val Thr Leu Ile Thr Ile
 1 5 10 15

Ile Ser Leu Glu Phe Ile Ile Gly Ile Leu Gly Asn Val Phe Ile Ala
 20 25 30

Leu Val Asn Ile Ile Asp Trp Val Lys Arg Gly Lys Ile Ser Ala Val
 35 40 45

Asp Lys Thr Tyr Met Ala Leu Ala Ile Ser Arg Thr Ala Phe Leu Leu
 50 55 60

Ser Leu Ile Thr Gly Phe Leu Val Ser Leu Leu Asp Pro Ala Leu Leu
 65 70 75 80

Gly Met Arg Thr Met Val Arg Leu Leu Thr Ile Ser Trp Met Val Thr
 85 90 95

Asn His Phe Ser Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe
 100 105 110

Leu Lys Ile Ala Asn Phe Ser Asn Ser Ile Phe Leu Val Leu Lys Trp
 115 120 125

Glu Ala Lys Lys Val Val Ser Val Thr Leu Val Val Ser Val Ile Ile
 130 135 140

Leu Ile Met Asn Ile Ile Val Ile Asn Lys Phe Thr Asp Arg Leu Gln
 145 150 155 160

Val Asn Thr Leu Gln Asn Cys Ser Thr Ser Asn Thr Leu Lys Asp Tyr
 165 170 175

Gly Leu Phe Leu Phe Ile Ser Thr Gly Phe Thr Leu Thr Pro Phe Ala
 180 185 190

Val Ser Leu Thr Met Phe Leu Leu Ile Phe Ser Leu Trp Arg His
 195 200 205

Leu Lys Asn Met Cys His Ser Ala Thr Gly Ser Arg Asp Val Ser Thr
 210 215 220

Val Ala His Ile Lys Gly Leu Gln Thr Val Val Thr Phe Leu Leu Leu
 225 230 235 240

Tyr Thr Ala Phe Val Met Ser Leu Leu Ser Glu Ser Leu Asn Ile Asn
245 250 255

Ile Gln His Thr Asn Leu Leu Ser His Phe Leu Arg Ser Ile Gly Val
260 265 270

Ala Phe Pro Thr Gly His Ser Cys Val Leu Ile Leu Gly Asn Ser Lys
275 280 285

Leu Arg Gln Ala Ser Leu Ser Val Ile Leu Trp Leu Arg Tyr Lys Tyr
290 295 300

Lys His Ile Glu Asn Trp Gly Pro
305 310

<210> 110
<211> 1484
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R03 (mGR03)

<400> 110
ctttaatagc agggtgtgaa tatTTaaatt ttctttctgc agcaactact gagggcttca 60
gactgctgta tacagggcat gaagcatctg gatgaagtgc agctgtgtgc cctttgacaa 120
caatttttg tggatgtgtg gagaacataa accatttcat tagtggaaatt tggctttgg 180
gtgacattgt ctatgatagt tctgaaagtgc attatgttaa gaatcagaca cagccgtcta 240
gaagattgtt ttaacacatc tttggtagtt cagaagaaaat tagatcatca tgggtgttgc 300
aataagggct attttatggg taacatttgc aactattata agtctggagt ttatcatagg 360
aatttttagga aatgtattca tagctctcgta gaacatcata gactgggtta aaagaggaaa 420
gatctctgca gtggataaga cctatatggc cctggccatc tccaggactg ctttttatt 480
gtcactaattc acagggttct tggtatcatt attggaccca gctttattgg gaatgagaac 540
gatggtaagg ctccttacta tttcctggat ggtgaccaat catttcagtg tctgggttgc 600
aacatgcctc agtatctttt atttctcaa gatacgtaat ttctcaattt ctatttcct 660
tggatctcaa tgggaagctaa aaaaagtggt atcagtgcata ttgggtgtat ctgtgataat 720
cttgatcatg aacattatag tcataaacaatttactgc acacttcag taaacacact 780
ccagaactgt agtacaagta acactttaaa agattatggg ctcttttat tcattagcac 840
tgggtttaca ctcacccat tcgctgtgtc tttgacaatg tttcttctgc tcattttctc 900
cctgtggaga catctgaaga atatgtgtca cagtgccaca ggctccagag atgtcagcac 960
agtggccac ataaaaggct tgcaaactgt ggtaacccatc ctgttactat atactgcttt 1020
tggatgtca cttctttcag agtctttgaa tattaacattt caacatataa atcttcttc 1080
tcattttta cggagtatag gagtagctt tcccacaggc cactcctgtg tactgattct 1140
tggaaacagt aagctgaggc aagcctctct ttctgtgtata ttgtggctga ggtataagta 1200
caaacatataa gagaattggg gcccctaaat catacagggtt atcctttcc acattctaga 1260
aaaaaatcg ttaataagaa caggaattt ggaaggaatc tggaaattatg aatctcatag 1320
gccatgaacc ttcagacaaa ggattcatc gagagataga gagagaacat tggatctgt 1380
aactcgacag gcaacactgt agattatgaa aataaatgtc agtctgtat gggaaagcaaa 1440
acatgctata ttttattaaat tgggtttgggt ttaagggtcgaaata 1484

<210> 111
<211> 302
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R04 (mGR04)

<400> 111
 Met Leu Ser Ala Leu Glu Ser Ile Leu Leu Ser Val Ala Thr Ser Glu
 1 5 10 15
 Ala Met Leu Gly Val Leu Gly Asn Thr Phe Ile Val Leu Val Asn Tyr
 20 25 30
 Thr Asp Trp Val Arg Asn Lys Lys Leu Ser Lys Ile Asn Phe Ile Leu
 35 40 45
 Thr Gly Leu Ala Ile Ser Arg Ile Phe Thr Ile Trp Ile Ile Thr Leu
 50 55 60
 Asp Ala Tyr Thr Lys Val Phe Leu Leu Thr Met Leu Met Pro Ser Ser
 65 70 75 80
 Leu His Glu Cys Met Ser Tyr Ile Trp Val Ile Ile Asn His Leu Ser
 85 90 95
 Val Trp Phe Ser Thr Ser Leu Gly Ile Phe Tyr Phe Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser His Tyr Ile Phe Leu Trp Met Lys Arg Arg Ala Asp Lys
 115 120 125
 Val Phe Val Phe Leu Ile Val Phe Leu Ile Ile Thr Trp Leu Ala Ser
 130 135 140
 Phe Pro Leu Ala Val Lys Val Ile Lys Asp Val Lys Ile Tyr Gln Ser
 145 150 155 160
 Asn Thr Ser Trp Leu Ile His Leu Glu Lys Ser Glu Leu Leu Ile Asn
 165 170 175
 Tyr Val Phe Ala Asn Met Gly Pro Ile Ser Leu Phe Ile Val Ala Ile
 180 185 190
 Ile Ala Cys Phe Leu Leu Thr Ile Ser Leu Trp Arg His Ser Arg Gln
 195 200 205
 Met Gln Ser Ile Gly Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His
 210 215 220
 Met Lys Ala Met Lys Val Leu Ile Ala Phe Ile Ile Leu Phe Ile Leu
 225 230 235 240
 Tyr Phe Leu Gly Ile Leu Ile Glu Thr Leu Cys Leu Phe Leu Thr Asn
 245 250 255
 Asn Lys Leu Leu Phe Ile Phe Gly Phe Thr Leu Ser Ala Met Tyr Pro
 260 265 270
 Cys Cys His Ser Phe Ile Leu Ile Leu Thr Ser Arg Glu Leu Lys Gln
 275 280 285
 Asp Thr Met Arg Ala Leu Gln Arg Leu Lys Cys Cys Glu Thr
 290 295 300

<210> 112
<211> 1529
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R04 (mGR04)

<210> 113
<211> 300
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R05 (mGR05)

<400> 113
Met Leu Ser Ala Ala Glu Gly Ile Leu Leu Ser Ile Ala Thr Val Glu
1 5 10 15

Ala Gly Leu Gly Val Leu Gly Asn Thr Phe Ile Ala Leu Val Asn Cys
 20 25 30

Met Asp Trp Ala Lys Asn Asn Lys Leu Ser Met Thr Gly Phe Leu Leu
35 40 45

Ile Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Leu Leu Thr Leu
 50 55 60

Asp Ala Tyr Ala Lys Leu Phe Tyr Pro Ser Lys Tyr Phe Ser Ser Ser
 65 70 75 80

Leu Ile Glu Ile Ile Ser Tyr Ile Trp Met Thr Val Asn His Leu Thr
 85 90 95
 Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser Asp Cys Val Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys
 115 120 125
 Ala Phe Val Phe Leu Leu Gly Cys Leu Leu Thr Ser Trp Val Ile Ser
 130 135 140
 Phe Ser Phe Val Val Lys Val Met Lys Asp Gly Lys Val Asn His Arg
 145 150 155 160
 Asn Arg Thr Ser Glu Met Tyr Trp Glu Lys Arg Gln Phe Thr Ile Asn
 165 170 175
 Tyr Val Phe Leu Asn Ile Gly Val Ile Ser Leu Phe Met Met Thr Leu
 180 185 190
 Thr Ala Cys Phe Leu Leu Ile Met Ser Leu Trp Arg His Ser Arg Gln
 195 200 205
 Met Gln Ser Gly Val Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His
 210 215 220
 Val Lys Ala Ile Lys Phe Leu Ile Ser Phe Ile Ile Leu Phe Val Leu
 225 230 235 240
 Tyr Phe Ile Gly Val Ser Ile Glu Ile Ile Cys Ile Phe Ile Pro Glu
 245 250 255
 Asn Lys Leu Leu Phe Ile Phe Gly Phe Thr Thr Ala Ser Ile Tyr Pro
 260 265 270
 Cys Cys His Ser Phe Ile Leu Ile Leu Ser Asn Ser Gln Leu Lys Gln
 275 280 285
 Ala Phe Val Lys Val Leu Gln Gly Leu Lys Phe Phe
 290 295 300

<210> 114
 <211> 903
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R05 (mGR05)

<400> 114
 atgctgagtg cggcagaagg catcctcctt tccattgcaa ctgttgaagc tgggctggga 60
 gttttaggga acacatttat tgcactggta aactgcattgg actggggccaa gaacaataag 120
 ctttctatga ctggcttcct tctcatcgcc ttagcaactt ccaggatttt tattgtgtgg 180
 ctattaactt tagatgcata tgcaaagctt ttctatccaa gtaagtattt ttcttagtagt 240
 ctgattgaaa tcatctctta tatatggatg actgtgaatc acctgactgt ctggtttgc 300
 accagcctaa gcatcttcta tttcctgaag atagccaatt ttccgactg tgtatttctc 360
 tgggtgaaga ggagaactga taaagcttt gttttctct tgggggtgttt gctaacttca 420
 tgggttaatct ccttctcatt tgggtgaag gtgtatgaagg acggtaaagt gaatcataga 480
 aacaggaccc tggagatgta ctgggagaaa agccaattca ctattaacta cgttttcctc 540

aatattggag tcatttctct ctttatgatg acctaactg catgttctt gttaattatg 600
tcacttggaa gacacagcag gcagatgcag tctgggttt caggattcag agaccta 660
acagaagctc atgtgaaaagc cataaaattt ttaatttcat ttatcatcct tttcgcttt 720
tattttatag gtgttcaat agaaattatc tgcatattha taccagaaaa caaactgcta 780
tttatttttggtttcaac tgcatccata tattcttgct gtcactcatt tattctaatt 840
ctatctaaca gccagctaaa gcaaggctt gtaaaggta 900
tag 903

<210> 115
<211> 308
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R06 (mGR06)

<400> 115
Met Leu Thr Val Ala Glu Gly Ile Leu Leu Cys Phe Val Thr Ser Gly
1 5 10 15
Ser Val Leu Gly Val Leu Gly Asn Gly Phe Ile Leu His Ala Asn Tyr
20 25 30
Ile Asn Cys Val Arg Lys Lys Phe Ser Thr Ala Gly Phe Ile Leu Thr
35 40 45
Gly Leu Ala Ile Cys Arg Ile Phe Val Ile Cys Ile Ile Ile Ser Asp
50 55 60
Gly Tyr Leu Lys Leu Phe Ser Pro His Met Val Ala Ser Asp Ala His
65 70 75 80
Ile Ile Val Ile Ser Tyr Ile Trp Val Ile Ile Asn His Thr Ser Ile
85 90 95
Trp Phe Ala Thr Ser Leu Asn Leu Phe Tyr Leu Leu Lys Ile Ala Asn
100 105 110
Phe Ser His Tyr Ile Phe Phe Cys Leu Lys Arg Arg Ile Asn Thr Val
115 120 125
Phe Ile Phe Leu Leu Gly Cys Leu Phe Ile Ser Trp Ser Ile Ala Phe
130 135 140
Pro Gln Thr Val Lys Ile Phe Asn Val Lys Lys Gln His Arg Asn Val
145 150 155 160
Ser Trp Gln Val Tyr Leu Tyr Lys Asn Glu Phe Ile Val Ser His Ile
165 170 175
Leu Leu Asn Leu Gly Val Ile Phe Phe Met Val Ala Ile Ile Thr
180 185 190
Cys Phe Leu Leu Ile Ile Ser Leu Trp Lys His Asn Arg Lys Met Gln
195 200 205
Leu Tyr Ala Ser Arg Phe Lys Ser Leu Asn Thr Glu Val His Val Lys
210 215 220

Val Met Lys Val Leu Ile Ser Phe Ile Ile Leu Leu Ile Leu His Phe
225 230 235 240

Ile Gly Ile Leu Ile Glu Thr Leu Ser Phe Leu Lys Tyr Glu Asn Lys
245 250 255

Leu Leu Leu Ile Leu Gly Leu Ile Ile Ser Cys Met Tyr Pro Cys Cys
260 265 270

His Ser Phe Ile Leu Ile Leu Ala Asn Ser Gln Leu Lys Gln Ala Ser
275 280 285

Leu Lys Ala Leu Lys Gln Leu Lys Cys His Lys Lys Asp Lys Asp Val
290 295 300

Arg Val Thr Trp
305

<210> 116
<211> 1242
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R06 (mGR06)

<400> 116
tatagttgca gcagaagcaa cgtagggat ctgttagagat gctgactgta gcagaaggaa 60
tcctcccttg tttttaact agtggttcag tcctgggagt tcttagaaat ggatttatcc 120
tgcacatcaaa ctacattaac tgtgtcagaa agaagttctc cacagctggc ttattctca 180
caggcttggc tatttgcaga atctttgtca tatgtataat aatctctgtat ggatatttaa 240
aattgttttc tccacatatg gttgcctctg atgcccacat tatagtgtatt tcttacatat 300
gggttaattat caatcataca agtataatgtt ttgccaccag cctcaacctc ttctatctcc 360
tgaagatagc aaatttttct cactacatct tcttctgctt gaagagaaga atcaatacag 420
tatttatctt tctcctgggta tgcttattta tatcatggtc aattgcttcc ccacaaacag 480
tgaagatatt taatgttaaa aagcagcaca gaaatgttcc ctggcagggtt tacctctata 540
agaatgagtt cattgtaagc cacattctc tcaacctggg agttatattc ttctttatgg 600
tggctatcat tacatgcttc ctattaatta tttcaactttt gaaacataac agaaagatgc 660
agttgtatgc ctcaagattc aaaagcctta acacagaagt acatgtgaaa gtcatgaaag 720
tttaattttc ttttattatc ctgttaatct tgcatttcat agggattttg atagaaacat 780
tgagctttttt aaaatatgaa aataaaactgc tacttattttt gggtttgata atttcatgca 840
tgtatccttg ctgtcattca tttatcctaa ttcttagcaaa cagtcagctg aagcaggctt 900
ctttgaaggc actgaagcaa ttaaaatgcc ataagaaaga caaggacgtc agagtgcacat 960
ggtagactta tggagaaatg aatggtcaca agaaatagcc tgggtgtggag atgttgatat 1020
ctctaaagac cgtttcactt ccaaattttt gcaatttattt aaaaaaaaaa gtcttgctga 1080
tatcatggaa tcatggaaaa tggtaattt gtgttttggg gacaggggtga ccagtgaagg 1140
tatggtaag cagcgaaaca ctcatacagc tcgttcgttc tttttgtatt ttatggat 1200
ttggtggccct tccaagacat gatttctcta tgtaagttt gg 1242

<210> 117
<211> 308
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R07 (mGR07)

<400> 117
 Met Leu Asn Ser Ala Glu Gly Ile Leu Leu Cys Val Val Thr Ser Glu
 1 5 10 15
 Ala Val Leu Gly Val Leu Gly Asp Thr Tyr Ile Ala Leu Phe Asn Cys
 20 25 30
 Met Asp Tyr Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Ile Leu
 35 40 45
 Ile Gly Leu Ala Ile Ser Arg Ile Gly Val Val Trp Ile Ile Ile Leu
 50 55 60
 Gln Gly Tyr Ile Gln Val Phe Phe Pro His Met Leu Thr Ser Gly Asn
 65 70 75 80
 Ile Thr Glu Tyr Ile Thr Tyr Ile Trp Val Phe Leu Asn His Leu Ser
 85 90 95
 Val Trp Phe Val Thr Asn Leu Asn Ile Leu Tyr Phe Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser Asn Ser Val Phe Leu Trp Leu Lys Arg Arg Val Asn Ala
 115 120 125
 Val Phe Ile Phe Leu Ser Gly Cys Leu Leu Thr Ser Trp Leu Leu Cys
 130 135 140
 Phe Pro Gln Met Thr Lys Ile Leu Gln Asn Ser Lys Met His Gln Arg
 145 150 155 160
 Asn Thr Ser Trp Val His Gln Arg Lys Asn Tyr Phe Leu Ile Asn Gln
 165 170 175
 Ser Val Thr Asn Leu Gly Ile Phe Phe Phe Ile Ile Val Ser Leu Ile
 180 185 190
 Thr Cys Phe Leu Leu Ile Val Phe Leu Trp Arg His Val Arg Gln Met
 195 200 205
 His Ser Asp Val Ser Gly Phe Arg Asp His Ser Thr Lys Val His Val
 210 215 220
 Lys Ala Met Lys Phe Leu Ile Ser Phe Met Val Phe Phe Ile Leu His
 225 230 235 240
 Phe Val Gly Leu Ser Ile Glu Val Leu Cys Phe Ile Leu Pro Gln Asn
 245 250 255
 Lys Leu Leu Phe Ile Thr Gly Leu Thr Ala Thr Cys Leu Tyr Pro Cys
 260 265 270
 Gly His Ser Ile Ile Val Ile Leu Gly Asn Lys Gln Leu Lys Gln Ala
 275 280 285
 Ser Leu Lys Ala Leu Gln Gln Leu Lys Cys Cys Glu Thr Lys Gly Asn
 290 295 300
 Phe Arg Val Lys
 305

<210> 118
<211> 1754
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R07 (mGR07)

<400> 118
ttcataatga agaggaggca gggcaatgtt ggtttctgtt gtctgaccag tgtatttgac 60
agtgatactc cacattgtat tgctaaatgc aaatagttcc aaaggaacaa gtaaaattta 120
tggaaatagaa gcttcttattt gcttattaaac aaactgcaag caaacattag tctgcacaca 180
ttttagatc aagctaaatc ttcaaaagca ataaaaaaga gcacccataa agttctgact 240
ctatcacatg acaataggct tggaaagatt gtctatgttag ataaagaaga tgccataact 300
tctccatcaa gaagccagta tatggacat tctccagcag ataatttaca atagatgcag 360
cagaagtaac ctttagagatc tggaaagatg ctgaattcag cagaaggcat cctcctttgt 420
gttgcacta gtgaggctgt gctcgagtt ttagggaca catatattgc accttttaac 480
tgcattggact atgctaagaa caagaagctc tctaagatcg gtttcattct cattggcttg 540
gcgatttcca gaatttgggtgt tggatggata ataattttac aagggtatata acaagtattt 600
tttccacaca tgcttacctc tggaaacata actgaatata ttacttacat atgggtattt 660
ctcaatcact taagtgtctg gtttgcacc aacctaaca tcctctactt tctaaagata 720
gctaattttt ccaactctgt atttctctgg ctggaaaggaa gaggtaatgc agtttttattt 780
tttctgtcag gatgcttact tacctcatgg ttactatgtt ttccacaaat gacaaagata 840
cttcaaaata gtaaaatgca ccagagaaac acatcttggg tccaccagcg gaaaaattac 900
tttcttattt accaaaagtgt gaccaatctg ggaatcttt tcttcattat tggatccctg 960
attacctgtt ttctgttgc tggagacatg tcagacaaat gcaactcagat 1020
gtttcaggat tcagagacca cagcacaaaa gtacatgtga aagctatgaa atttctaata 1080
tcttttatgg tcttctttat tctgcattt gtggccttt ccatagaatg gctatgctt 1140
attctgcac aaaaataact gctcttata actgggttga cagccacatg cctctatccc 1200
tgcggtaact caatcatcgt aatttttagga aataaggatg taaagcaagc ctctttgaag 1260
gcactgcagc aactaaaatg ctgtgagaca aaaggaaattt tcagactcaa ataaaatgggt 1320
ttgcaataa atagctgcct tggatccca ctgtttta ccctgttagt tgatgtttagt 1380
aaaaagttcct gctatgggttga atgacatctc aagaatcta tttttctggg ggcatgttaa 1440
gtccacgtga agcctcaactt catactgtga ctgtgactatg caaattctt ccacaaaata 1500
accagataac attcagcctg gagataaattt catttaaagg cttttatggt gaggataaac 1560
aaaaaaaaaa aatcattttt ctgtgatca ctgtactcc caggatgatg aaaaagaaaac 1620
aagacaaatg gttgtgatca gcctttgtgt gtcttagacag agctaggac cagatgtga 1680
tgcttgcgtt tggatccca agttattgcc tctctgccat tcggatttcc 1740
tcaggtgaga attc 1754

<210> 119
<211> 297
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R08 (mGR08)

<400> 119
Met Leu Trp Glu Leu Tyr Val Phe Val Phe Ala Ala Ser Val Phe Leu
1 5 10 15
Asn Phe Val Gly Ile Ile Ala Asn Leu Phe Ile Ile Val Ile Ile Ile
20 25 30
Lys Thr Trp Val Asn Ser Arg Arg Ile Ala Ser Pro Asp Arg Ile Leu
35 40 45
Phe Ser Leu Ala Ile Thr Arg Phe Leu Thr Leu Gly Leu Phe Leu Leu
50 55 60

Asn Ser Val Tyr Ile Ala Thr Asn Thr Gly Arg Ser Val Tyr Phe Ser			
65	70	75	80
Thr Phe Phe Leu Leu Cys Trp Lys Phe Leu Asp Ala Asn Ser Leu Trp			
85	90	95	
Leu Val Thr Ile Leu Asn Ser Leu Tyr Cys Val Lys Ile Thr Asn Phe			
100	105	110	
Gln His Pro Val Phe Leu Leu Leu Lys Arg Thr Ile Ser Met Lys Thr			
115	120	125	
Thr Ser Leu Leu Leu Ala Cys Leu Leu Ile Ser Ala Leu Thr Thr Leu			
130	135	140	
Leu Tyr Tyr Met Leu Ser Gln Ile Ser Arg Phe Pro Glu His Ile Ile			
145	150	155	160
Gly Arg Asn Asp Thr Ser Phe Asp Leu Ser Asp Gly Ile Leu Thr Leu			
165	170	175	
Val Ala Ser Leu Val Leu Asn Ser Leu Leu Gln Phe Met Leu Asn Val			
180	185	190	
Thr Phe Ala Ser Leu Leu Ile His Ser Leu Arg Arg His Ile Gln Lys			
195	200	205	
Met Gln Arg Asn Arg Thr Ser Phe Trp Asn Pro Gln Thr Glu Ala His			
210	215	220	
Met Gly Ala Met Arg Leu Met Ile Cys Phe Leu Val Leu Tyr Ile Pro			
225	230	235	240
Tyr Ser Ile Ala Thr Leu Leu Tyr Leu Pro Ser Tyr Met Arg Lys Asn			
245	250	255	
Leu Arg Ala Gln Ala Ile Cys Met Ile Ile Thr Ala Ala Tyr Pro Pro			
260	265	270	
Gly His Ser Val Leu Leu Ile Ile Thr His His Lys Leu Lys Ala Lys			
275	280	285	
Ala Lys Lys Ile Phe Cys Phe Tyr Lys			
290	295		

<210> 120
 <211> 1475
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R08 (mGR08)

<400> 120
 aagcttgttt gtaatttaggc attcctaaga aaataagaac aggagtgaag aaatagtaat 60
 ttaatccttg aaagatttgc atctcagtaa aagcagctgc ctcttagacc agaaaatggtg 120
 tttgccatgc tggaaaataa aaaggagacc tcttccagg ctgcattctg tgtctgctta 180
 cttatttcag tttgtttca tcggcaccaa acgaggaaag atgctctggg aactgtatgt 240
 atttgtgttt gctgcctcgg tttttttaaa ttttgttagga atcattgcaa atctatttat 300
 tatagtgata attattaaga cttgggtcaa cagtcgcaga attgcctctc cgataggat 360

cctgttcagc ttggccatca ctagattcct gactttgggg ttgtttctac tgaacagtgt 420
 ctacattgct acaaatactg gaaggcgtact ctactttcc acatttttc tattgtgtg 480
 gaagtttctg gatgcaaaca gtctctgggtt agtgcattt ctgaacagct tgtattgtt 540
 gaagattact aattttcaac acccagtttctt tctcctgtt aaacggacta tctctatgaa 600
 gaccaccagc ctgctgttgg cctgtcttctt gatttcagcc ctcaccactc tccttatatta 660
 tatgtctctca cagatatac gttttctgaa acacataatt gggagaaaatg acacgtcatt 720
 tgacctcagt gatggatct tgacgttagt agccttttgc gtcctgaact cacttctaca 780
 gtttatgctc aatgtgactt ttgccttctt gttaatacat tccttgagaa gacatataca 840
 gaagatgcag agaaaacagga ccagcttttgc gaatccccag acggaggctc acatgggtgc 900
 tatgaggctg atgatcttttgc tctcgtgtt ctacatttcca tattcaatttgc ctaccctgtt 960
 ctatcttcctt tccttatgaa ggaagaatct gagagcccg gccatttgca tgattattac 1020
 tgctgttctac cctccaggac attctgttctt cctcatttac acacatcata aactgaaagc 1080
 taaagcaaaag aagattttctt gtttctacaatgtt gtagcagaat ttctttagt gtttacagca 1140
 tcaatttcatttgc gtttgggttgc attagaaatg tctcgtgtt ctacatttcca tattcaatttgc 1200
 tcttggatctt ggcatttcatttgc cccttgcatttgc aagtgcatttgc attttgggtca atacagcatttgc 1260
 ttttggctaa tattttaaag taaatcacaat tccataagaa attgtttaag ggattttacgt 1320
 atttttcatg gctatcacaat tccatagacaa tgaaatcacat ctttttttttgc ctttttttttgc 1380
 tgaagtttacca gggggaaatgtc catgaatgaa ggcacatttgc tgatgttctt ggttagcaca 1440
 gatttagagaa tttggcctca actgagcaag atatc 1475

<210> 121
 <211> 316
 <212> PRT
 <213> Mus sp.

<220>
 <223> mouse T2R09 (mGR09)

<400> 121	121														
Met	Glu	His	Leu	Leu	Lys	Arg	Thr	Phe	Asp	Ile	Thr	Glu	Asn	Ile	Leu
1										10				15	
Leu	Ile	Ile	Leu	Phe	Ile	Glu	Leu	Ile	Ile	Gly	Leu	Ile	Gly	Asn	Gly
														30	
Phe	Thr	Ala	Leu	Val	His	Cys	Met	Asp	Trp	Val	Lys	Arg	Lys	Lys	Met
35								40				45			
Ser	Leu	Val	Asn	Lys	Ile	Leu	Thr	Ala	Leu	Ala	Thr	Ser	Arg	Ile	Phe
50						55				60					
Leu	Leu	Trp	Phe	Met	Leu	Val	Gly	Phe	Pro	Ile	Ser	Ser	Leu	Tyr	Pro
65						70				75				80	
Tyr	Leu	Val	Thr	Thr	Arg	Leu	Met	Ile	Gln	Phe	Thr	Ser	Thr	Leu	Trp
								85		90			95		
Thr	Ile	Ala	Asn	His	Ile	Ser	Val	Trp	Phe	Ala	Thr	Cys	Leu	Ser	Val
								100		105			110		
Phe	Tyr	Phe	Leu	Lys	Ile	Ala	Asn	Phe	Ser	Asn	Ser	Pro	Phe	Leu	Tyr
115								120				125			
Leu	Lys	Arg	Arg	Val	Glu	Lys	Val	Val	Ser	Val	Thr	Leu	Leu	Val	Ser
130								135				140			
Leu	Val	Leu	Leu	Phe	Leu	Asn	Ile	Leu	Leu	Leu	Asn	Leu	Glu	Ile	Asn
145								150				155			160

Met Cys Ile Asn Glu Tyr His Gln Ile Asn Ile Ser Tyr Ile Phe Ile
 165 170 175
 Ser Tyr Tyr His Leu Ser Cys Gln Ile Gln Val Leu Gly Ser His Ile
 180 185 190
 Ile Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu
 195 200 205
 Leu Ile Phe Ser Leu Trp Thr Leu His Lys Arg Met Gln Gln His Val
 210 215 220
 Gln Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln
 225 230 235 240
 Ala Val Ile Ala Phe Leu Leu Leu Tyr Ser Ile Phe Ile Leu Ser Leu
 245 250 255
 Leu Leu Gln Phe Trp Ile His Gly Leu Arg Lys Lys Pro Pro Phe Ile
 260 265 270
 Ala Phe Cys Gln Val Val Asp Thr Ala Phe Pro Ser Phe His Ser Tyr
 275 280 285
 Val Leu Ile Leu Arg Asp Arg Lys Leu Arg His Ala Ser Leu Ser Val
 290 295 300
 Leu Ser Trp Leu Lys Cys Arg Pro Asn Tyr Val Lys
 305 310 315

<210> 122
 <211> 1339
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R09 (mGR09)

<400> 122
 gaattcagaa atcatcaaaa aatcttcaaa actacatgtt taaaatagca cttcaaatga 60
 atacatttgc aaatctttac aactaataca taaaatggag catctttga agagaacatt 120
 tgatatcacc gagaacatac ttctaattat tttatttcatt gaattaataa ttggacttat 180
 agggaaacgga ttcacagcct tggtcactg catggactgg gttaaagagaa aaaaaatgtc 240
 attagttaat aaaatcctca ccgctttggc aacttctaga atttcctgc tctggttcat 300
 gcttagtaggt tttccaatta gctcactgta cccatattta gttactacta gactgatgat 360
 acagttcact agtactctat ggactatagc taaccatatt agtgtctggg ttgctacatg 420
 cctcagtgtc ttttattttc tcaagatagc caattttct aattctcctt ttctctatct 480
 aaagaggaga gttggaaaag tagttcagt tacattactg gtgtctctgg tcctcttg 540
 tttaaatatt ttactactta atttggaaat taacatgtgt ataaatgaat atcatcaa 600
 aaacatatac tacatcttca tttcttattt ccatttaagt tgtcaaattc aggtgttagg 660
 aagtcacatt atttcctgt ctgtccccgt tgggtgtcc ctgtcaactt ttctcctg 720
 catcttctcc ctgtggacac ttccacaagag gatgcagcag catgttcagg gaggcagaga 780
 tgccagaacc acggcccaact tcaaagcctt gcaaggcagtg attgccttgc tcctactata 840
 ctccatttt atcctgtcac tgttactaca atttggatc catggattaa ggaagaaacc 900
 tcctttcatt gcattttgtc aggttgtaga tacagctttt ctttcattcc attcatatgt 960
 cttgattctg agagacagga agctgagaca cgcctctc tctgtgttgc cgtggctgaa 1020
 atgcaggcca aattatgtga aataatattt ctttgtatc tcattttcaa ttttaaaaata 1080
 ttcttagaat ttgactgcat gtatttcatc ttttatttga aacaaccact aattaaagct 1140
 attactaatt tagcaagtcg tatacaaggt tatttttaa tacacatatac aaaaactgac 1200
 atgtttatgt tctacaaaaa cctgaatata tcaaaattat ataaattttg tatcaacgat 1260

taacaatgga gttttttat ttatgacctg tcacgggact ccggtgaggc cagcttgtca 1320
gatgaaagtc tgaaagctt 1339

<210> 123
<211> 333
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R10 (mGR10)

<400> 123
Met Phe Ser Gln Ile Ile Ser Thr Ser Asp Ile Phe Thr Phe Thr Ile
1 5 10 15
Ile Leu Phe Val Glu Leu Val Ile Gly Ile Leu Gly Asn Gly Phe Ile
20 25 30
Ala Leu Val Asn Ile Met Asp Trp Thr Lys Arg Arg Ser Ile Ser Ser
35 40 45
Ala Asp Gln Ile Leu Thr Ala Leu Ala Ile Thr Arg Phe Leu Tyr Val
50 55 60
Trp Phe Met Ile Ile Cys Ile Leu Leu Phe Met Leu Cys Pro His Leu
65 70 75 80
Leu Thr Arg Ser Glu Ile Val Thr Ser Ile Gly Ile Ile Trp Ile Val
85 90 95
Asn Asn His Phe Ser Val Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
100 105 110
Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
115 120 125
Trp Arg Val Lys Lys Val Val Leu Met Ile Ile Gln Val Ser Met Ile
130 135 140
Phe Leu Ile Leu Asn Leu Leu Ser Leu Ser Met Tyr Asp Gln Phe Ser
145 150 155 160
Ile Asp Val Tyr Glu Gly Asn Thr Ser Tyr Asn Leu Gly Asp Ser Thr
165 170 175
Pro Phe Pro Thr Ile Ser Leu Phe Ile Asn Ser Ser Lys Val Phe Val
180 185 190
Ile Thr Asn Ser Ser His Ile Phe Leu Pro Ile Asn Ser Leu Phe Met
195 200 205
Leu Ile Pro Phe Thr Val Ser Leu Val Ala Phe Leu Met Leu Ile Phe
210 215 220
Ser Leu Trp Lys His His Lys Lys Met Gln Val Asn Ala Lys Pro Pro
225 230 235 240
Arg Asp Ala Ser Thr Met Ala His Ile Lys Ala Leu Gln Thr Gly Phe
245 250 255

Ser Phe Leu Leu Leu Tyr Ala Val Tyr Leu Leu Phe Ile Val Ile Gly
260 265 270

Met Leu Ser Leu Arg Leu Ile Gly Gly Lys Leu Ile Leu Leu Phe Asp
275 280 285

His Ile Ser Gly Ile Gly Phe Pro Ile Ser His Ser Phe Val Leu Ile
290 295 300

Leu Gly Asn Asn Lys Leu Arg Gln Ala Ser Leu Ser Val Leu His Cys
305 310 315 320

Leu Arg Cys Arg Ser Lys Asp Met Asp Thr Met Gly Pro
325 330

<210> 124
<211> 1371
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R10 (mGR10)

<400> 124
gaattcaaca tcttattcaa cttcagaaaa ctggatatta gacacagtgt ctggatgaag 60
cagaggtat ctctttggaa aaaaaagcca agtagtcata aagaatttat gaaacaattc 120
ctgggattgt ttatatttgt tacaaacaaa tttatatgtt tgtagtcag taatgtataa 180
gtgggatttt aaagcatgtat tatcttgaat ttttacaaa aaacatgtat tgctttttaa 240
atgttagcaga aacattaaaa attgaagcat gttctcacag ataataagca ccagtgtat 300
ttttactttt acaataatat tatttgttga attagtaata ggaatttttag gaaatggatt 360
catagcacta gtgaatatca tggactggac caagagaaga agcatttcat cagcggatca 420
gattctcaact gcttggcca ttaccagatt tctctatgtg tggtttatga tcatttgtat 480
attgttatttc atgctgtgcc cacatttgct tacaagatca gaaatagtaa catcaattgg 540
tattattttgg atagtgataa accatttcag cgtttggctt gccacatgcc tcggtgtctt 600
ttatatttctg aagataggca attttctaa ctctttgttt ctttaccaa atggagagt 660
taaaaaagta gtttaatga taatacaggt atcaatgatt ttcttgattt taaacctgtt 720
atctctaaggc atgtatgatc agttctcaat tgatgtttat gaaggaaata catcttataa 780
tttagggat tcaaccccat ttcccacaat ttcccttattc atcaatttcat caaaagttt 840
cgtaatcacc aactcatccc atatttctt acccatcaac tccctgttca tgctcataacc 900
cttcacagtg tccctggtag ctttctcat gctcatctc tcactgtgga agcatcacaa 960
aaagatgcag gtcaatgcca aaccacctag agatgccagc accatggccc acattaaagg 1020
cttgcacaca gggttctcct tcctgctgct gtatgcagta tacttacttt ttattgtcat 1080
aggaatgtt agccttaggt tgataggagg aaaattaata cttttattt accacatttc 1140
tggaaatagg tttcctataa gccactcatt tggctgatt ctggaaata acaagctgag 1200
acaagccagt ctttcagtgt tgcattgtct gaggtgccga tccaaagata tggacaccat 1260
gggtccataa aaaatttcag aggtcattgg gaaacattt gagatcttat agggaaaaaa 1320
aaaaatgtgg ggcttcaaag ctggtaggag taatatacag aaggatagga g 1371

<210> 125
<211> 303
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R11 (mGR11)

<220>
<221> MOD_RES
<222> (169)
<223> Xaa = any amino acid

<400> 125
Met Glu His Pro Leu Arg Arg Thr Phe Asp Phe Ser Gln Ser Ile Leu
1 5 10 15

Leu Thr Ile Leu Phe Ile Glu Leu Ile Ile Gly Leu Ile Arg Asn Gly
20 25 30

Leu Met Val Leu Val His Cys Ile Asp Trp Val Lys Arg Lys Lys Phe
35 40 45

His Leu Leu Ile Lys Ser Ser Pro Leu Trp Gln Thr Ser Arg Ile Cys
50 55 60

Leu Leu Trp Phe Met Leu Ile His Leu Leu Ile Thr Leu Leu Tyr Ala
65 70 75 80

Asp Leu Ala Ser Thr Arg Thr Met Met Gln Phe Ala Ser Asn Pro Trp
85 90 95

Thr Ile Ser Asn His Ile Ser Ile Trp Leu Ala Thr Cys Leu Gly Val
100 105 110

Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Thr Phe Leu Tyr
115 120 125

Leu Lys Trp Arg Val Gln Phe Leu Leu Asn Ile Leu Leu Val Lys
130 135 140

Phe Glu Ile Asn Met Trp Ile Asn Glu Tyr His Gln Ile Asn Ile Pro
145 150 155 160

Tyr Ser Phe Ile Ser Tyr Tyr Gln Xaa Cys Gln Ile Gln Val Leu Ser
165 170 175

Leu His Ile Ile Phe Leu Ser Val Pro Phe Ile Leu Ser Leu Ser Thr
180 185 190

Phe Leu Leu Ile Phe Ser Leu Trp Thr Leu His Gln Arg Met Gln
195 200 205

Gln His Val Gln Gly Tyr Arg Asp Ala Ser Thr Met Ala His Phe Lys
210 215 220

Ala Leu Gln Ala Val Ile Ala Phe Leu Leu Ile His Ser Ile Phe Ile
225 230 235 240

Leu Ser Leu Leu Leu Gln Leu Trp Lys His Glu Leu Arg Lys Lys Pro
245 250 255

Pro Phe Val Val Phe Cys Gln Val Ala Tyr Ile Ala Phe Pro Ser Ser
260 265 270

His Ser Tyr Val Phe Ile Leu Gly Asp Arg Lys Leu Arg Gln Ala Cys
275 280 285

Leu Ser Val Leu Trp Arg Leu Lys Cys Arg Pro Asn Tyr Val Gly
290 295 300

<210> 126
<211> 1108
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R11 (mGR11)

<400> 126
aataatgtat gtggaagagt taagtataaa tggatgtatga gaatgaactc agaaaatcatc 60
aaaaatctt aaaactgcat gttaaaaatc acacttcaaa tgaatataatt tggatattctt 120
tagaactaat aaataaaaatg gaggcatcatt tgaggagaac atttgatttc tcccgagaca 180
tacttctaac cattttattc attgaattaa taattggact tataagaat ggattaatgg 240
tattggcga ctgcatacat tgggttaaga gaaaaaaatt tcattttgtta atcaaattcc 300
caccactttg gcaaaacttcc agaatttgtc tgctctgggt catgctaata catctcctga 360
ttactttattt gtatgcagat ttagcttagta ctagaacgat gatgcaattc gctagcaatc 420
catggactat atctaaccat atcagcatct ggcttgctac atgccttggt gtctttttt 480
ttctcaagat agccaatttt tctaactcta cttttctcta tctaaaatgg cgagttcagt 540
tcctcttgc ttatattttt ctgggttaat ttgagattaa catgtggata aatgaatatc 600
atcaaataaa cataccatac agtttcattt ttatttacca aattgtcaaa tacaggtgtt 660
aagtcttcac attatttcc tggatgtccc ctttatttttgc tccctgtcaa cttttctcc 720
gctcatcttc tccctgtgga cacttcacca gaggatgcag cagcatgttc aaggatacag 780
agatgccagc acaatggccc acttcaaagc cttgcaagca gtgattgcct ttctcttaat 840
acactccatt ttatccctgt cactgttact acaactttgg aaacatgaat taaggaagaa 900
acctcctttt gttgtatttt gtcagggtgc atatatacgat tttccttcat cccatttcata 960
tgtcttcatt ctgggagaca gaaagctgag acaggcttgc ctctctgtgt tggaggct 1020
gaaatgcagg ccaaattatg tggataaaa tctcttgc tttcatttc caattcttaa 1080
atattctttt attttgcataaaattt 1108

<210> 127
<211> 150
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R12 (mGR12)

<400> 127
Gly Ala Ile Val Asn Val Asp Phe Leu Ile Gly Asn Val Gly Asn Gly
1 5 10 15
Phe Ile Val Val Ala Asn Ile Met Asp Leu Val Lys Arg Arg Lys Leu
20 25 30
Ser Ser Val Asp Gln Leu Leu Thr Ala Leu Ala Val Ser Arg Ile Thr
35 40 45
Leu Leu Trp Tyr Leu Tyr Ile Met Lys Arg Thr Phe Leu Val Asp Pro
50 55 60
Asn Ile Gly Ala Ile Met Gln Ser Thr Arg Leu Thr Asn Val Ile Trp
65 70 75 80
Ile Ile Ser Asn His Phe Ser Ile Trp Leu Ala Thr Thr Leu Ser Ile
85 90 95

Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Ile Phe Cys Tyr
100 105 110

Leu Arg Trp Arg Phe Glu Lys Val Ile Leu Met Ala Leu Leu Val Ser
115 120 125

Leu Val Leu Leu Phe Ile Asp Ile Leu Val Thr Asn Met Tyr Ile Asn
130 135 140

Ile Trp Thr Asp Glu Phe
145 150

<210> 128

<211> 520

<212> DNA

<213> Mus sp.

<220>

<223> mouse T2R12 (mGR12)

<400> 128
ttttcagcag tgactttggg aagcagaacg tcctcttaga gacagttgggt gctgctatcc 60
tagttaatgt ggagaatag ttaatgttgg a tttcttaatt gggaaatgttgg ggaatggatt 120
cattgttggc gcaaacataa tggacttggt caagagaaga aagcttctt cagtggatca 180
gctgctcaact gcactggccg tctccagaat cactttgctg tggtaacctgt acataatgaa 240
acgaacatatt ttagtggatc caaacatgg tgcaattatg caatcaacaa gactgactaa 300
tgttatctgg ataatttcta accattttag tatatggctg gccaccaccc tcagcatctt 360
ttatttctc aagatagcaa attttctaa ctcttatttc tgttacctga ggtggagatt 420
tgaaaaggtg attttggatgg cattgcttggt gtccttggtc ctcttggtta tagatatttt 480
agtaacaaac atgtacatttta atatttggac tgatgaattc 520

<210> 129

<211> 309

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R13 (mGR13)

<400> 129
Met Val Ala Val Leu Gln Ser Thr Leu Pro Ile Ile Phe Ser Met Glu
1 5 10 15

Phe Ile Met Gly Thr Leu Gly Asn Gly Phe Ile Phe Leu Ile Val Cys
20 25 30

Ile Asp Trp Val Gln Arg Arg Lys Ile Ser Leu Val Asp Gln Ile Arg
35 40 45

Thr Ala Leu Ala Ile Ser Arg Ile Ala Leu Ile Trp Leu Ile Phe Leu
50 55 60

Asp Trp Trp Val Ser Val His Tyr Pro Ala Leu His Glu Thr Gly Lys
65 70 75 80

Met Leu Ser Thr Tyr Leu Ile Ser Trp Thr Val Ile Asn His Cys Asn
85 90 95

Phe Trp Leu Thr Ala Asn Leu Ser Ile Leu Tyr Phe Leu Lys Ile Ala
100 105 110

Asn Phe Ser Asn Ile Ile Phe Leu Tyr Leu Lys Phe Arg Ser Lys Asn
115 120 125

Val Val Leu Val Thr Leu Leu Val Ser Leu Phe Phe Leu Phe Leu Asn
130 135 140

Thr Val Ile Ile Lys Ile Phe Ser Asp Val Cys Phe Asp Ser Val Gln
145 150 155 160

Arg Asn Val Ser Gln Ile Phe Ile Met Tyr Asn His Glu Gln Ile Cys
165 170 175

Lys Phe Leu Ser Phe Thr Asn Pro Met Phe Thr Phe Ile Pro Phe Val
180 185 190

Met Ser Thr Val Met Phe Ser Leu Leu Ile Phe Ser Leu Trp Arg His
195 200 205

Leu Lys Asn Met Gln His Thr Ala Lys Gly Cys Arg Asp Ile Ser Thr
210 215 220

Thr Val His Ile Arg Ala Leu Gln Thr Ile Ile Val Ser Val Val Leu
225 230 235 240

Tyr Thr Ile Phe Phe Leu Ser Phe Phe Val Lys Val Trp Ser Phe Val
245 250 255

Ser Pro Glu Arg Tyr Leu Ile Phe Leu Phe Val Trp Ala Leu Gly Asn
260 265 270

Ala Val Phe Ser Ala His Pro Phe Val Met Ile Leu Val Asn Arg Arg
275 280 285

Leu Arg Leu Ala Ser Leu Ser Leu Ile Phe Trp Leu Trp Tyr Arg Phe
290 295 300

Lys Asn Ile Glu Val
305

<210> 130

<211> 1199

<212> DNA

<213> Mus sp.

<220>

<223> mouse T2R13 (mGR13)

<400> 130

aagcttgttt gtgtttggat gaattctatt tatgtctatc aatttaagat tttcatatga 60
atcattaaga aatcttgata gttgttgtg agatatcact tctgcaattt ttaaatgaaa 120
ttacactcat attttgaagg aacaataatgt tttaaaggaa tatattaaca aatcttcagc 180
agttacacctca gaagtttggg tattgttta cagaaaatgg tggcagttct acagagcaca 240
cttccaataa ttttcagtat ggaattcata atgggaacct taggaaatgg attcattttt 300
ctgatagtc gcatagactg ggtccaaaga agaaaaatct cttagtgg tcaaattccgc 360
actgctctgg caat tagcag aatcgctcta atttgggtga tattcctaga ttgggtgggtg 420
tctgttcatt acccagcatt acatgaaact ggtaagatgt tatcaacata ttgatttcc 480
tggacgggtga tcaatcattt gtaacttttgg cttaactgcaa acttggcat cctttatgg 540

ctcaagatag ccaactttc taacattatt tttctttatc taaagtttag atctaaaaat 600
gtggatttag tgaccctgtt agtgtctta ttttcttgc tcttaatac tgtaattata 660
aaaatatttt ctgatgtgtg ttttgcata gttcaaagaa atgtgtctca aattttcata 720
atgtataacc atgaacaaat ttgtaaattt cttccctta ctaaccctat gttcacattc 780
atacctttt ttagtccac ggtaatgtt tcttgcata tcttctccct gtggagacat 840
ctgaagaata tgcagcacac cgccaaagga tgcagagaca tcagcacac agtgcacatc 900
agagccctgc aaaccatcat tggatgtgtc gtgcataca ctatttttt tctatcattt 960
tttggatgg tttggatgtt tggatgtgtc gagagatacc tgatctttt gtttgcgtgg 1020
gctctggaa atgctgtttt ttctgcata ccatttgcata tgatctttt gtttgcgtgg 1080
ttgagattgg cttctcttc tctgattttt tggatgtgtc acaggttaa aatataagaa 1140
gtatagggtc caaagaccac caaggaatca tttccttat cctaaagaaa aatcaggag 1199

<210> 131
<211> 309
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R14 (mGR14)

<400> 131
Met Leu Ser Thr Met Glu Gly Val Leu Leu Ser Val Ser Thr Ser Glu
1 5 10 15

Ala Val Leu Gly Ile Val Gly Asn Thr Phe Ile Ala Leu Val Asn Cys
20 25 30

Met Asp Tyr Asn Arg Asn Lys Lys Leu Ser Asn Ile Gly Phe Ile Leu
35 40 45

Thr Gly Leu Ala Ile Ser Arg Ile Cys Leu Val Leu Ile Leu Ile Thr
50 55 60

Glu Ala Tyr Ile Lys Ile Phe Tyr Pro Gln Leu Leu Ser Pro Val Asn
65 70 75 80

Ile Ile Glu Leu Ile Ser Tyr Leu Trp Ile Ile Ile Cys Gln Leu Asn
85 90 95

Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
100 105

Asn Phe Ser His Tyr Ile Phe Val Trp Leu Lys Arg Arg Ile Asp Leu
115 120 125

Val Phe Phe Phe Leu Ile Gly Cys Leu Leu Ile Ser Trp Leu Phe Ser
130 135 140

Phe Pro Val Val Ala Lys Met Val Lys Asp Asn Lys Met Leu Tyr Ile
145 150 155 160

Asn Thr Ser Trp Gln Ile His Met Lys Lys Ser Glu Leu Ile Ile Asn
165 170 175

Tyr Val Phe Thr Asn Gly Gly Val Phe Leu Phe Phe Met Ile Met Leu
180 185 190

Ile Val Cys Phe Leu Leu Ile Ile Ser Leu Trp Arg His Arg Arg Gln
195 200 205

Met Glu Ser Asn Lys Leu Gly Phe Arg Asp Leu Asn Thr Glu Val His
210 215 220

Val Arg Thr Ile Lys Val Leu Leu Ser Phe Ile Ile Leu Phe Ile Leu
225 230 235 240

His Phe Met Gly Ile Thr Ile Asn Val Ile Cys Leu Leu Ile Pro Glu
245 250 255

Ser Asn Leu Leu Phe Met Phe Gly Leu Thr Thr Ala Phe Ile Tyr Pro
260 265 270

Gly Cys His Ser Leu Ile Leu Ile Leu Ala Asn Ser Arg Leu Lys Gln
275 280 285

Cys Ser Val Met Ile Leu Gln Leu Leu Lys Cys Cys Glu Asn Gly Lys
290 295 300

Glu Leu Arg Asp Thr
305

<210> 132
<211> 1535
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R14 (mGR14)

<400> 132
ctgcaggtat atacctaccc tgaaggcttc atctagagta aacaaagtag tctgtatagt 60
ctgccattcc tcagattctc ctcaacttcc caccctccag tgaccttct ccttttctac 120
agtcaaaacta tggacacctac aacctgacac ttcttcagat gcaaaatatt ctcacagaga 180
caagtaaaac atacaaaaca aatactttaa tttgcctatt aacaaatggc aagaaaagat 240
tcaggcttga acatcctgt a gacaagctaa ggacaggagc aactgaaggg atctccatga 300
agaccttca gatttctacc aaaagtaatt ttaactata ttaagtctt taaagaaaaga 360
aagtaaagcc actctttat tgaacagcaa tagattggaa tcttaaacaa ctgcaacaga 420
agccatttta aagatcaaca aagatgctga gcacaatggc aggtgtcctc ctttcagttt 480
caactagtga ggctgtctg ggcattgttag ggaacacatt cattgcactt gtaaactgt 540
tggactataa caggaacaag aagctctta atattggctt tattctcact ggcttggcaa 600
tttccagaat ttgccttgc ttgatctta tcacagaggg atacataaaa atattctatc 660
cacagttgt gtctcctgtc aacataattt agctcatcag ttatctatgg ataattatct 720
gtcaattgaa tgtctggttt gccactagtc tcagttttt ttatccctg aagatagcaa 780
attttccca ctacatattt gtctggtaa aaagaagaat tgatttagtt ttttcttcc 840
tgataggggtg cttgttatac tcatggctat tttttttccc agttgtgc aagatggta 900
aagataataa aatgctgtat ataaacacat cttggcagat ccacatgaag aaaagtgagt 960
taatcattaa ctatgtttc accaatgggg gagatttttt atttttatg ataatgttaa 1020
ttgtatgttt cctgttaatc atttcacattt ggagacatcg caggcagatg gaatcaaata 1080
aattaggatt cagagatctc aacacagaag ttcatgtgag aacaataaaa gttttattgt 1140
cttttattat cttttttata ttgcatttca tgggtattac cataaaatgtt atttgtctgt 1200
taatcccaga aagcaacttg ttattcatgt ttgggttgac aactgcattc atctatcccg 1260
gctgccactc acttacccaa attctagcaa acagtcggct gaagcagtgc tctgtatgt 1320
tactgcaact attaaagtgc tgtgagaatg gtaaagaact cagagacaca tgacagtctg 1380
gaacacatgc aatctggaat tgtcagtgaa aaaagttact gaagatctt tcacttgac 1440
tatgctctt tattgatttgc gcatcattat caaacactgt tggagcccttg tgaactctg 1500
ttcagagtttctc aaggaatcac actcc 1535

<210> 133
<211> 310
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R15 (mGR15)

<400> 133
Met Cys Ala Val Leu Arg Ser Ile Leu Thr Ile Ile Phe Ile Leu Glu
1 5 10 15
Phe Phe Ile Gly Asn Leu Gly Asn Gly Phe Ile Ala Leu Val Gln Cys
20 25 30
Met Asp Leu Arg Lys Arg Arg Thr Phe Pro Ser Ala Asp His Phe Leu
35 40 45
Thr Ala Leu Ala Ile Ser Arg Leu Ala Leu Ile Trp Val Leu Phe Leu
50 55 60
Asp Ser Phe Leu Phe Ile Gln Ser Pro Leu Leu Met Thr Arg Asn Thr
65 70 75 80
Leu Arg Leu Ile Gln Thr Ala Trp Asn Ile Ser Asn His Phe Ser Ile
85 90 95
Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Leu Phe Lys Ile Ala Ile
100 105 110
Phe Ser Asn Tyr Leu Phe Phe Tyr Leu Lys Arg Arg Val Lys Arg Val
115 120 125
Val Leu Val Ile Leu Leu Leu Ser Met Ile Leu Leu Phe Phe Asn Ile
130 135 140
Phe Leu Glu Ile Lys His Ile Asp Val Trp Ile Tyr Gly Thr Lys Arg
145 150 155 160
Asn Ile Thr Asn Gly Leu Ser Ser Asn Ser Phe Ser Glu Phe Ser Arg
165 170 175
Leu Ile Leu Ile Pro Ser Leu Met Phe Thr Leu Val Pro Phe Gly Val
180 185 190
Ser Leu Ile Ala Phe Leu Leu Ile Phe Ser Leu Met Lys His Val
195 200 205
Arg Lys Met Gln Tyr Tyr Thr Lys Gly Cys Lys Asp Val Arg Thr Met
210 215 220
Ala His Thr Thr Ala Leu Gln Thr Val Val Ala Phe Leu Leu Tyr
225 230 235 240
Thr Thr Phe Phe Leu Ser Leu Val Val Glu Val Ser Thr Leu Glu Met
245 250 255
Asp Glu Ser Leu Met Leu Leu Phe Ala Lys Val Thr Ile Met Ile Phe
260 265 270

Pro Ser Ile His Ser Cys Ile Phe Ile Leu Lys His Asn Lys Leu Arg
275 280 285

Gln Asp Leu Leu Ser Val Leu Lys Trp Leu Gln Tyr Trp Cys Lys Arg
290 295 300

Glu Lys Thr Leu Asp Ser
305 310

<210> 134
<211> 1482
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R15 (mGR15)

<400> 134
aataatagat ttttaatat tcagaatttt taagtaatgt agtattgtta gcagcatagc 60
ttataggaaa agttccaagt aattttgatt ttgttaattct gattccccca aatcaagtat 120
caagtttacc tgcacagaca agggaagaag tggcaaattg tgcaaattgag agcaacttta 180
tttgactgtc agtacgttga aattcagttt ttcttaatc agttatggat tgacatttt 240
gtgcacagaa ccttggaaagaa tttcagccaa gctggaggtt aaaatccaaa attctgatga 300
taaaaacccaaa agtaaatcac agttaatct tctttatttt tcttttttaa tactgtatata 360
ggacattttt taatacagca tattttttt ttgaaattta gaaaaaaaaacc actaagaaat 420
attcaccaat ggaatagact ttaaagtccac ttagagaatg tttgtctttc tacgttagcat 480
actgacaatc attttcattt tggagttctt cattggaaat ctggggaaatg gattcatagc 540
tctggtacaa tgcattggact tacgaaagag aagaacgttc ctttcagcag atcatttcct 600
cactgctctg gccatctcca ggcttgctt gatatgggtt ttatattctt tagtattttctt 660
gtttatacaa tccccattac tgatgactag aaatacatta agactgattc agactgcctg 720
gaatataagc aatcatttca gtatatgtt tgctaccagc ctcagcatct tttatctt 780
caagatagcc atttttcttca actatctttt ctcttacctg aagcggagag tttttttttt 840
ggttttgggtt atactgctgc tatccatgtt cttttgtttt ttaatataat ttttagaaat 900
caaacatatt gatgtcttgg tctatggaaac caaaagaaac ataactaatg gtttgagttc 960
aaacagttt tcagagttt ccaggcttat ttaattcca agttaatgt tcacatttagt 1020
accctttgggtt gtatccttga tagctttctt cctcctaatc tttccctta taaaacatgt 1080
aaggaagatg cagtaactaca ccaaaggatg cttttttttt tttttttttt tttttttttt 1140
agccctgcag actgtgggtt ctttccttctt attatatact actttctttc tttttttttt 1200
tgtggaaattt tcaacacttg aaatggatga aagtctgtatg tttttttttt tttttttttt 1260
tataatgatt tttcccttca tccactctt tttttttttt tttttttttt tttttttttt 1320
acaggacttg ctttcagttt tttttttttt tttttttttt tttttttttt tttttttttt 1380
ggattcatag accattgtat gcatcacctt gaatattcta gagggtgtt gttttttttt 1440
aaagtattga atttttaat ttgacccctt tttttttttt tttttttttt tttttttttt 1482

<210> 135
<211> 305
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R16 (mGR16)

<400> 135
Met Asn Gly Val Leu Gln Val Thr Phe Ile Val Ile Leu Ser Val Glu
1 5 10 15

Phe Ile Ile Gly Ile Phe Gly Asn Gly Phe Ile Ala Val Val Asn Ile
20 25 30

Lys Asp Leu Val Lys Gly Arg Lys Ile Ser Ser Val Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Ala Ile Ser Arg Ile Ala Leu Leu Trp Leu Ile Leu Val
 50 55 60

Ser Trp Trp Ile Phe Val Leu Tyr Pro Gly Gln Trp Met Thr Asp Arg
 65 70 75 80

Arg Val Ser Ile Met His Ser Ile Trp Thr Thr Phe Asn Gln Ser Ser
 85 90 95

Leu Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
 100 105 110

Asn Phe Ser Asn Pro Ile Phe Leu Tyr Leu Lys Val Arg Leu Lys Lys
 115 120 125

Val Met Ile Gly Thr Leu Ile Met Ser Leu Ile Leu Phe Cys Leu Asn
 130 135 140

Ile Ile Ile Met Asn Ala Pro Glu Asn Ile Leu Ile Thr Glu Tyr Asn
 145 150 155 160

Val Ser Met Ser Tyr Ser Leu Ile Leu Asn Asn Thr Gln Leu Ser Met
 165 170 175

Leu Phe Pro Phe Ala Asn Thr Met Phe Gly Phe Ile Pro Phe Ala Val
 180 185 190

Ser Leu Val Thr Phe Val Leu Leu Val Phe Ser Leu Trp Lys His Gln
 195 200 205

Arg Lys Met Gln His Ser Ala His Gly Cys Arg Asp Ala Ser Thr Lys
 210 215 220

Ala His Ile Arg Ala Leu Gln Thr Leu Ile Ala Ser Leu Leu Leu Tyr
 225 230 235 240

Ser Ile Phe Phe Leu Ser His Val Met Lys Val Trp Ser Ala Leu Leu
 245 250 255

Leu Glu Arg Thr Leu Leu Leu Ile Thr Gln Val Ala Arg Thr Ala
 260 265 270

Phe Pro Ser Val His Ser Trp Val Leu Ile Leu Gly Asn Ala Lys Met
 275 280 285

Arg Lys Ala Ser Leu Tyr Val Phe Leu Trp Leu Arg Cys Arg His Lys
 290 295 300

Glu
 305

<210> 136
 <211> 1316
 <212> DNA
 <213> Mus sp.

<220>

<223> mouse T2R16 (mGR16)

<400> 136

tttatgtatgg aaagaataaa accattagca aggcttaatg gcttgttgg tattagacct 60
gtacattgtt tatggaacat gatatggagc tttgttatt gaatatgcac aatattttag 120
aagcatgtt caaagaatct taagtaatta caatagaaat tgaagcatcc aagtgaagat 180
gaatgggtgc ctacaggta catttatagt cattttgagt gtggaaattna taattggcat 240
cttggcaat ggattcatag cggtggtgaa cataaaggac ttggtcaagg gaaggaagat 300
ctcttcagtg gatcagatcc tcactgctc ggccatctcc agaattgcac tgctgtgggt 360
aatatttagta agttggtgaa tatttgtgct ttacccagga caatggatga ctgatagaag 420
agtttagcata atgcacagta tatggacaac attcaaccag agtagtctct ggtttgctac 480
aagtctcagc atctttattt ttttcaagat agcaaatttt tccaacccta tttttcttta 540
tttaaaggc agactaaaaa aagtcatgtat agggacattt ataatgtctt tgattctctt 600
ttgtttaaatt attatcatta tgaatgcacc tgagaacatt ttaatcaactg aatataatgt 660
atctatgtct tacagcttga ttttgaataa cacacagctt tctatgtgt ttccatttgc 720
caacaccatg tttgggttca tacctttgc tgtgtcaactg gtcacttttgc ttcttcttgc 780
tttctccctg tggaaacatc agagaaagat gcaacacagt gcccattggat gcaagagatgc 840
cagcaactaag gcccacatca gaggcatttgc gacattgatt gctccctcc tcctgttattc 900
cattttcttc ctgtctcatg ttatgaaggt ttggagtgtct ctgcttctgg agaggacact 960
cctgcttttg atcacacagg ttgcaagaac agctttccg tcagtgcact cctgggtccct 1020
gattctgggc aatgctaaga tgagaaaggc ttctctctat gtattctgt ggttgaggtg 1080
caggcacaaa gaatgaaacc ctacagtgtt cagacctggg gatatattt gtggatgatc 1140
ttacatatct tagagggaaa tggattaaaaa gaaattctca tatttataaa ttttttaggtc 1200
tgaattacat aaaaatgtat ataatatttt caaagtacaa gatagtagtt tataacttac 1260
atgataaataa ctgtctatgc atcttcttagt cttttagaa tatgtaaaaa catgtt 1316

<210> 137

<211> 330

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R17 (mGR17)

<400> 137

Met Lys His Phe Trp Lys Ile Leu Ser Val Ile Ser Gln Ser Thr Leu
1 5 10 15

Ser Val Ile Leu Ile Val Glu Leu Val Ile Gly Ile Ile Gly Asn Gly
20 25 30

Phe Met Val Leu Val His Cys Met Asp Trp Val Lys Lys Lys Lys Met
35 40 45

Ser Leu Val Asn Gln Ile Leu Thr Ala Leu Ser Ile Ser Arg Ile Phe
50 55 60

Gln Leu Cys Leu Leu Phe Ile Ser Leu Val Ile Asn Phe Ser Tyr Thr
65 70 75 80

Asp Leu Thr Thr Ser Ser Arg Met Ile Gln Val Met Tyr Asn Ala Trp
85 90 95

Ile Leu Ala Asn His Phe Ser Ile Trp Ile Ala Thr Cys Leu Thr Val
100 105 110

Leu Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Phe Phe Leu Tyr
115 120 125

Leu Lys Trp Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser
 130 135 140
 Leu Leu Leu Ile Leu Asn Ile Leu Leu Thr Asn Leu Glu Thr Asp
 145 150 155 160
 Met Trp Thr Asn Glu Tyr Gln Arg Asn Ile Ser Cys Ser Phe Ser Ser
 165 170 175
 His Tyr Tyr Ala Lys Cys His Arg Gln Val Leu Arg Leu His Ile Ile
 180 185 190
 Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu Leu
 195 200 205
 Ile Phe Ser Leu Trp Thr His His Lys Arg Met Gln Gln His Val Gln
 210 215 220
 Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln Thr
 225 230 235 240
 Val Ile Ala Phe Phe Leu Leu Tyr Ser Ile Phe Ile Leu Ser Val Leu
 245 250 255
 Ile Gln Ile Trp Lys Tyr Glu Leu Leu Lys Lys Asn Leu Phe Val Val
 260 265 270
 Phe Cys Glu Val Val Tyr Ile Ala Phe Pro Thr Phe His Ser Tyr Ile
 275 280 285
 Leu Ile Val Gly Asp Met Lys Leu Arg Gln Ala Cys Leu Pro Leu Cys
 290 295 300
 Ile Ile Ala Ala Glu Ile Gln Thr Thr Leu Cys Arg Asn Phe Arg Ser
 305 310 315 320
 Leu Lys Tyr Phe Arg Leu Cys Cys Ile Phe
 325 330

<210> 138
 <211> 1354
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R17 (mGR17)

<400> 138
 gaattctgg ctggcacccc tgagctgtgt gagtagacac attatcatgg aaagagattc 60
 agaatctgtc actgtcaaaa ctgcatgttt gctcctctgt tagtgtgtt gggaaagttt 120
 agaaaaataac attttatgg aatcaactca gaggttgc aaaaattgtcg aaacagcattt 180
 taaaaaattt acatctcaac tggatataatg agcaagtctt tataactgtat atataaaaatg 240
 aagcactttt ggaagatatt atctgttatac tcccagagca cactttcagt cattttatc 300
 gtggaaattttt taatttggat tataggaaat gggttcatgg tcctggtcca ctgtatggac 360
 tgggttaaga aaaagaaaaat gtcccttagtt aatcaaattt ttactgcttt gtcaatctcc 420
 agaatttttc agctctgtttt attgtttata agtttagtaa tcaactttt atatacagat 480
 ttaactacaa gttcaaggat gatacaagtc atgtacaatg cttggattttt agccaaaccat 540
 ttcagcatct ggattgctac atgcctcaact gtccttttattt ttctaaagat agccaaattttt 600
 tctaactttt tttttcttta tctaaagtgg agagttggaa aagtagtttc agttacactg 660
 ttgggtgtcat tgctcctcctt gattttaaat attttactaa ctaacttggaa aaccgacatg 720

tggacaaatg aatatcaaag aaacatatca tgtagcttca gtttcattt ctagcaaag 780
 tgcacaggc aggtgttaag gttcacatt atttctgt ctgtccccgt tggttgc 840
 ctgtcaactt ttctctgtc catcttctcc ctgtggacac atcacaagag gatgcagc 900
 catgttcagg gaggcagaga tgccagaacc acggccact tcaaagccct acaaactgtg 960
 attgcatttt tcctactata ttccatttt attctgtctg tcttaataca aatttgaaa 1020
 tatgaattac tgaagaaaaa tctttcggt gtatggatg aggttgata tatagtttt 1080
 ccgacattcc attcatatat tctgattgtt ggagacatga agctgagaca ggcctgcctg 1140
 cctctctgtt ttatcgacg taaaatttca actacactat gtagaaattt tagatcacta 1200
 aagtacttta gattatgtt tatattctt aaaaaatttactgataaaatca atgtctttt 1260
 tattttcat tttaaatatc tttaatttt gactgcatga aattgatttc tgcttgcaat 1320
 tatcactgat taaaactatt aataattaa ctag 1354

<210> 139

<211> 299

<212> PRT

<213> Mus sp.

<220>

<223> mouse T2R18 (mGR18)

<400> 139

Met Val Pro Thr Gln Val Thr Ile Phe Ser Ile Ile Met Tyr Val Leu
 1 5 10 15

Glu Ser Leu Val Ile Ile Val Gln Ser Cys Thr Thr Val Ala Val Leu
 20 25 30

Phe Arg Glu Trp Met His Phe Gln Arg Leu Ser Pro Val Glu Thr Ile
 35 40 45

Leu Ile Ser Leu Gly Ile Ser His Phe Cys Leu Gln Trp Thr Ser Met
 50 55 60

Leu Tyr Asn Phe Gly Thr Tyr Ser Arg Pro Val Leu Leu Phe Trp Lys
 65 70 75 80

Val Ser Val Val Trp Glu Phe Met Asn Ile Leu Thr Phe Trp Leu Thr
 85 90 95

Ser Trp Leu Ala Val Leu Tyr Cys Val Lys Val Ser Ser Phe Thr His
 100 105 110

Pro Ile Phe Leu Trp Leu Arg Met Lys Ile Leu Lys Leu Val Leu Trp
 115 120 125

Leu Ile Leu Gly Ala Leu Ile Ala Ser Cys Leu Ser Ile Ile Pro Ser
 130 135 140

Val Val Lys Tyr His Ile Gln Met Glu Leu Val Thr Leu Asp Asn Leu
 145 150 155 160

Pro Lys Asn Asn Ser Leu Ile Leu Arg Leu Gln Gln Phe Glu Trp Tyr
 165 170 175

Phe Ser Asn Pro Leu Lys Met Ile Gly Phe Gly Ile Pro Phe Phe Val
 180 185 190

Phe Leu Ala Ser Ile Ile Leu Leu Thr Val Ser Leu Val Gln His Trp
 195 200 205

Val Gln Met Lys His Tyr Ser Ser Ser Asn Ser Ser Leu Lys Ala Gln
210 215 220

Phe Thr Val Leu Lys Ser Leu Ala Thr Phe Phe Thr Phe Phe Thr Ser
225 230 235 240

Tyr Phe Leu Thr Ile Val Ile Ser Phe Ile Gly Thr Val Phe Asp Lys
245 250 255

Lys Ser Trp Phe Trp Val Cys Glu Ala Val Ile Tyr Gly Leu Val Cys
260 265 270

Ile His Phe Thr Ser Leu Met Met Ser Asn Pro Ala Leu Lys Lys Ala
275 280 285

Leu Lys Leu Gln Phe Trp Ser Pro Glu Pro Ser
290 295

<210> 140
<211> 2887
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R18 (mGR18)

<220>
<221> modified_base
<222> (1083)
<223> n = g, a, c or t

<400> 140
gcgtgcttca cagagcagta tactacaaag caaatgtcat tgctgccatt gtatatttct 60
ctaaagacat ttcacatttt atctccctgt cccattgtgt gcagagccca cacttcaatc 120
aatcaattcc ttaattataa gctattgttt cattatttca ttcctacgt ttttttgcatt 180
ttttactaaa actccaaagc agacatttc taattataat cctacatgtt gttagaattt 240
taaaaattat atactatttt ctttgcacca ctgagttcag taggtttga aggtttatgc 300
ttaacaattt aacatttcat gttagattat tcctgccttc ctaatcttga ataattaaat 360
gtccatccag gcttagaatt cacagagtc acagcttca ccttgattct ctcactatct 420
atcaatgact agaatctgtc tgcactttt gaaaccgcta attaaatagt tggtgcttat 480
ttaaagggtt ccccatgcca agagaaaatg tatttcttct cttagatgcct tcgtcccttta 540
caagttacat gcttactga tggtaattt gtttcttcc agttcatctg ggttaagtga 600
cctaagaacc tagccatggc aggagaaaaca gaagcaaata ttaacgatac aagaacaagt 660
tccagaacat tggaaagtac ttagtaaagg catttggattt agcaaaaagaa tagtagcgaa 720
gcaaaaaata cttcatctcc attgggaggtt caagaaaagac tatgcagtgt ttttgatgca 780
acttgcattc tctgagttt acgattcagc acacactttt gagatttgcac ttcaacaggt 840
ggagccagca gacctgagct ttaggaatgt tggtaattt tccaagcaaa gacttccgtt 900
accttttgc tgccttca caattcggtt gcaatgtca caccgccccaa ctgttggaaat 960
gcttgggaaa agggattctg agactggcat tagtatgtca tttgacagaa tggaaacatt 1020
gcccaggggca ttaatgcaca gtaaaggatt caccttttct aagtgcctaa attttaaatt 1080
tgnatatttt tagaaagacat tattttaaaag aaagggtggag aggatatacca aacagcacct 1140
tgagcagata aagaggtgaa gaagaaaaaa caacatgcgtt acatgtatgg tttcttcttta 1200
tgaaaaatgtt caaatgtatct taggatcaag aatccacacc tgaatgagat ttgcttgcatt 1260
ccctgtgtga atttgcattt acaagcaaaag cacagacaaa tgctgttagat agggaaatgt 1320
ctatgtcaaa tgcgtgttaag gaggatttgc atccacaaaag aagtgccttc ttatactgag 1380
agtgcataaa acacatgtcc gtttcatattt cgaaaaagtgg tataagatgtt ttgacttctt 1440
ggcttaggaag agacttcaga gtggaaagcat ggtgccaacg caagtcacca tcttctccat 1500
catcatgtat tgcgtgttagt ctttagtaat aattgtgcaaa agttgcacaa cggttgcagt 1560
gctattcaga gatgtggatgc actttcaaaag actgtcaccg gtggagacga ttctcatcag 1620
cctggggcatc tcacatttctt gtcgtacatgtt gacatcaatgtt ctatacaact ttggtaactt 1680

ttcttaggcct gtcctttat tttggaaggt atcagtcgtc tgggagttca tgaacatttt 1740
 gacattctgg ttaaccagg ggcttgctgt cctctactgt gtcaaggctct cttccttcac 1800
 tcaccccatc ttcctctggc tgaggatgaa aatctgaaa ctggttctct ggttatact 1860
 ggtgtctctg atagttctt gttgtcaat catccctct gttgttaaat atcacatcca 1920
 gatggaatta gtcaccctag ataatttacc caagaacaat tctttgattc taagactaca 1980
 acagttgaa tggattttt ctaatcctt aaaaatgatt ggctttggta ttcctttctt 2040
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 gaaacactac agcagcagca actccagcct gaaagcttag ttcaactgttc tgaagtctct 2160
 tgctaccttc ttcacccctt tcacatccta ttttctgact atagtcatct ccttatttg 2220
 cactgtgttt gataagaat cttggttctg ggtctgcga gctgtcatct atggtttagt 2280
 ctgtattcac ttcacttcac tgatgatgag caaccctgcga ttgaaaaagg cactgaagct 2340
 gcagttctgg agcccagagc cttcctgagg caggaaacac agttaagcct ctagggtaag 2400
 gagactttgc attggcacag tccctatagt gtaatgcaaa cttgaacaca aacttcatcc 2460
 ctttcacat ccacaaatgg ctgcacatcatc acatcatcac cagtctccc tgattctga 2520
 cccattctct tcctgtccta tccatagtc ccaggttggg tttgattttt ctcatgatca 2580
 caccaactct gcttagctt tgccaccact gtaatgtaa acatggggtg ttctatataat 2640
 tacagtcaaa atcattctca cattgttgat tgccctcacaa attcatataa atcccccttc 2700
 ctgtcaggaa tttattgtct gctcactaa tgctcaccat atattaaagc cattaattcc 2760
 cccttcctac cttgagttt agaaggaaaa tgtcttacca ttgcccacaa cctattctgc 2820
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 aaacaac 2887

<210> 141
 <211> 335
 <212> PRT
 <213> Mus sp.

<220>
 <223> mouse T2R19 (mGR19)

<400> 141
 Met Met Glu Gly His Met Leu Phe Phe Leu Leu Val Val Val Val Gln
 1 5 10 15

Phe Leu Thr Gly Val Leu Ala Asn Gly Leu Ile Val Val Val Asn Ala
 20 25 30

Ile Asp Leu Ile Met Trp Lys Lys Met Ala Pro Leu Asp Leu Leu Leu
 35 40 45

Phe Cys Leu Ala Thr Ser Arg Ile Ile Leu Gln Leu Cys Ile Leu Phe
 50 55 60

Ala Gln Leu Gly Leu Ser Cys Leu Val Arg His Thr Leu Phe Ala Asp
 65 70 75 80

Asn Val Thr Phe Val Tyr Ile Asn Glu Leu Ser Leu Trp Phe Ala
 85 90 95

Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Ile Ala Thr Ile Pro His
 100 105 110

Pro Leu Phe Leu Trp Leu Lys Met Arg Ile Ser Arg Leu Val Pro Trp
 115 120 125

Leu Ile Leu Ala Ser Val Val Tyr Val Thr Val Thr Thr Phe Ile His
 130 135 140

Ser Arg Glu Thr Ser Glu Leu Pro Lys Gln Ile Phe Ile Ser Phe Phe
 145 150 155 160

Ser Lys Asn Thr Thr Arg Val Arg Pro Ala His Ala Thr Leu Leu Ser
165 170 175

Val Phe Val Phe Gly Leu Thr Leu Pro Phe Leu Ile Phe Thr Val Ala
180 185 190

Val Leu Leu Leu Ser Ser Leu Trp Asn His Ser Arg Gln Met Arg
195 200 205

Thr Met Val Gly Thr Arg Glu Pro Ser Arg His Ala Leu Val Ser Ala
210 215 220

Met Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Leu Ser His Asp Met
225 230 235 240

Val Ala Val Leu Ile Cys Thr Gln Gly Leu His Phe Gly Ser Arg Thr
245 250 255

Phe Ala Phe Cys Leu Leu Val Ile Gly Met Tyr Pro Ser Leu His Ser
260 265 270

Ile Val Leu Ile Leu Gly Asn Pro Lys Leu Lys Arg Asn Ala Lys Thr
275 280 285

Phe Ile Val His Cys Lys Cys Cys His Cys Ala Arg Ala Trp Val Thr
290 295 300

Ser Arg Asn Pro Arg Leu Ser Asp Leu Pro Val Pro Ala Thr His His
305 310 315 320

Ser Ala Asn Lys Thr Ser Cys Ser Glu Ala Cys Ile Met Pro Ser
325 330 335

<210> 142
<211> 1698
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R19 (mGR19)

<400> 142
ctgcagccta gagaactaat gcataggaaa cttatattcc caccccggtg acgtcactct 60
gacagaagtg aacttatatt cccacccctcg tgacgtcaact ctgacagaag tgacttgtt 120
ttgtatgatg ctccaggatg cctcattagc attgaggaca atcataatta agtaaggcaa 180
ggcatgaagg tggcctcac taggtacctg gaggttctg gttgcatgat ttacttgta 240
tgactctgac acttaagaag acctgaaaaa tgcaaaagct gtcataaggc acagttcggt 300
tctatggat ctcttcctta tttgactgac attgagttga gaaggcagca ctataaacaa 360
atgggccccca ctttcctctt ccattgtctt tgggttggca tcatctccaa aggaaccttg 420
gtctagttga aagaagccag aaatcataca tggctgagac tgtgcataac tctatgtatc 480
attnaaagaa gtcattgggtt cttcttattt taaaatgtatg gaaggtcata tgctcttctt 540
ccttcggcgt gttttttttt acgttttaac tgggttctt gcaaatggcc tcattgtgg 600
tgtcaatgcc atcgacttga tcatgtggaa gaaaatggcc ccactggatc tgcttcttt 660
ttgcctggcg acttctcgga tcattctca attgtgtata ttgtttgcac agctgggtct 720
atccctgtttt gttttttttt gttttttttt tgacaaatgtt acctttgtct acattataaa 780
cgaactgagt ctctggttt ccacatggct tgggttttc tactgtgcca agattgctac 840
catccctcac ccactctttc tgggttggaa gatgaggata tccaggttgg tgccatggct 900
gatcctggca tctgtggctt atgttaactgt tactactttc atccatagca gagagacttc 960
agaacttcctt aagcaaatct ttataagctt tttttctaaa aataacaactc gggtcagacc 1020
agcgcatgcc acactactct cagtctttgtt ctttggctc acactaccat ttctcatctt 1080

cactgttgct gttctgctct tgggtgcctc cctgtggAAC cacagccggc agatgaggac 1140
 tatgggtggAA actaggAAC ctagcagaca tgccctcgTC aGTGCGATGC tctccattTC 1200
 gtcattccCTC atccCTCTAC tctccatGA catggtagCT gttctgatCT gtacCCAAAG 1260
 CCTCCACTT ggaAGcAGAA CCTTGcATT CTGCTTATTG gttattggTA tGTACCCCTC 1320
 cttacactG attgtcttaA ttttaggAAA ccctaAGctG aaacgaaATG caaaaACgtT 1380
 cattgtccat tgtaagtGTT gtcattGTC aagagCTTGG gtcacCTCAA ggaACCCAAg 1440
 actcagcGac ttGCCAGtGC ctGCTACTCA tcactcAGCC aacaAGACAT CCTGCTCAGA 1500
 agcctgtata atGCCATCTT aattgtcAA cctGAGGCTT aatCATTCA aagggtAAAT 1560
 tGatgtatCAA agCCCAACAC atGATATGAC atcaAGGTCC atatCCAGT agtcatGTGG 1620
 aaataccacc ttGCAAAATG atGTCATTGA gaaACCAGGG caaaatggagt cttaggtCTT 1680
 cagtatgatt tgctgcAG 1698

<210> 143
 <211> 295
 <212> PRT
 <213> Mus sp.

<220>
 <223> mouse T2R20 (mGR20)

<400> 143
 Met Asn Leu Val Glu Trp Ile Val Thr Ile Ile Met Met Thr Glu Phe
 1 5 10 15

 Leu Leu Gly Asn Cys Ala Asn Val Phe Ile Thr Ile Val Asn Phe Ile
 20 25 30

 Asp Cys Val Lys Arg Arg Lys Ile Ser Ser Ala Asp Arg Ile Ile Thr
 35 40 45

 Ala Ile Ala Ile Phe Arg Ile Gly Leu Leu Trp Ala Met Leu Thr Asn
 50 55 60

 Trp His Ser His Val Phe Thr Pro Asp Thr Asp Asn Leu Gln Met Arg
 65 70 75 80

 Val Phe Gly Gly Ile Thr Trp Ala Ile Thr Asn His Phe Thr Thr Trp
 85 90 95

 Leu Gly Thr Ile Leu Ser Met Phe Tyr Leu Phe Lys Ile Ala Asn Phe
 100 105 110

 Ser Asn Ser Leu Phe Leu His Leu Lys Arg Lys Leu Asp Asn Val Leu
 115 120 125

 Leu Val Ile Phe Leu Gly Ser Ser Leu Phe Leu Val Ala Tyr Leu Gly
 130 135 140

 Met Val Asn Ile Lys Lys Ile Ala Trp Met Ser Ile His Glu Gly Asn
 145 150 155 160

 Val Thr Thr Lys Ser Lys Leu Lys His Val Thr Ser Ile Thr Asn Met
 165 170 175

 Leu Leu Phe Ser Leu Ile Asn Ile Val Pro Phe Gly Ile Ser Leu Asn
 180 185 190

 Cys Val Leu Leu Leu Ile Tyr Ser Leu Ser Lys His Leu Lys Asn Met
 195 200 205

Lys Phe Tyr Gly Lys Gly Cys Gln Asp Gln Ser Thr Met Val His Ile
210 215 220

Lys Ala Leu Gln Thr Val Val Ser Phe Leu Leu Leu Tyr Ala Thr Tyr
225 230 235 240

Ser Ser Cys Val Ile Ile Ser Gly Trp Ser Leu Gln Asn Ala Pro Val
245 250 255

Phe Leu Phe Cys Val Thr Ile Gly Ser Phe Tyr Pro Ala Gly His Ser
260 265 270

Cys Ile Leu Ile Trp Gly Asn Gln Lys Leu Lys Gln Val Phe Leu Leu
275 280 285

Leu Leu Arg Gln Met Arg Cys
290 295

<210> 144
<211> 1394
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R20 (mGR20)

<400> 144
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aaaatttcac taacaaattt ttgactgcc aataataatga aggtttaaag aaagaacaac 120
atttgaagca atggaccaga attcctctt atttgactct tagcaaattg gaatgcagca 180
tccttcaag agcagcactg aaatatacca gtcaatggca gagagtaaaa aagtatgcaa 240
ttggagacat tatggtaata taaattcca taaaaatga gactgcattc acctattaca 300
acacattgct attctgctca acacagagtt aaaaagaaac aagaactctt gtatacattc 360
agttagtcac aagtataatt atgttccat attttaaaaa aatgaatcat gatctgtgaa 420
ttgagcctgg cttttttgc ctctctctt ttattcttt ccttagaca gacacaatga 480
atttggtaga atggattgtt accatcataa tgatgacaga atttctctt gaaaaactgtg 540
ccaatgtctt cataaccata gtgaacttca tcgactgtgt gaagagaaga aagatctcct 600
cagctgatcg aattataact gctattgcc tcttcagaat tggtttggat tggcaatgt 660
taacgaactg gcattcacat gtgttactc cagacacaga caatttacaa atgagagtt 720
tcggtggaat tacctggct ataaccaacc atttaccac ttggctgggg accatactga 780
gcatgtttt tttattcaag atagccaatt tttccaacag tctatttctt catctaaaaa 840
gaaaacttga caatgttcta cttgtgattt tcctggatc gtctctgtt ttgggtgcat 900
atcttggat ggtgaacatc aagaagattg ctggatgag tattcatgaa gaaaaatgtga 960
ccacaaagag caaactgaag catgtAACAA gcatcacaaa tatgcttctc ttcagcctga 1020
taaacattgt accatttggat atatcactga actgtgttct gctcttaatc tattccctga 1080
gtaaacatct caagaatatg aaattctatg gcaaggatg tcaagatcag agcaccatgg 1140
tccacataaa ggccttgc aactgtgttctt ctttctctt gttatatgcc acataactctt 1200
cctgtgtcat tataatcaggt tggagttgc aaaatgcacc agtcttcctg ttttgtgtga 1260
caattggatc cttctaccca gcaggtcatt ctgttatctt gatttggggaa aaccagaaac 1320
ttaaacaggt cttctgttg ttgctgaggc agatgagatg ctgactgaaa aaatgaaagt 1380
ccccctgtct ctag 1394

<210> 145
<211> 305
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R21 (mGR21)

<400> 145

Met Gly Ser Asn Val Tyr Gly Ile Leu Thr Met Val Met Ile Ala Glu
1 5 10 15

Phe Val Phe Gly Asn Met Ser Asn Gly Phe Ile Val Leu Ile Asn Cys
20 25 30

Ile Asp Trp Val Arg Lys Gly Thr Leu Ser Ser Ile Gly Trp Ile Leu
35 40 45

Leu Phe Leu Ala Ile Ser Arg Met Val Leu Ile Trp Glu Met Leu Ile
50 55 60

Thr Trp Ile Lys Tyr Met Lys Tyr Ser Phe Ser Phe Val Thr Gly Thr
65 70 75 80

Glu Leu Arg Gly Ile Met Phe Thr Trp Val Ile Ser Asn His Phe Ser
85 90 95

Leu Trp Leu Ala Thr Ile Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
100 105 110

Ser Phe Ser Lys Pro Val Phe Leu Tyr Leu Lys Trp Arg Glu Lys Lys
115 120 125

Val Leu Leu Ile Val Leu Leu Gly Asn Leu Ile Phe Leu Met Leu Asn
130 135 140

Ile Leu Gln Ile Asn Lys His Ile Glu His Trp Met Tyr Gln Tyr Glu
145 150 155 160

Arg Asn Ile Thr Trp Ser Ser Arg Val Ser Asp Phe Ala Gly Phe Ser
165 170 175

Asn Leu Val Leu Leu Glu Met Ile Val Phe Ser Val Thr Pro Phe Thr
180 185 190

Val Ala Leu Val Ser Phe Ile Leu Leu Ile Phe Ser Leu Trp Lys His
195 200 205

Leu Gln Lys Met His Leu Asn Ser Arg Gly Glu Arg Asp Pro Ser Thr
210 215 220

Lys Ala His Val Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu
225 230 235 240

Tyr Ala Thr Tyr Phe Ile Ser Phe Phe Leu Ser Leu Ile Pro Met Ala
245 250 255

His Lys Thr Arg Leu Gly Leu Met Phe Ser Ile Thr Val Gly Leu Phe
260 265 270

Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly His Ser Asn Leu
275 280 285

Arg Gln Ala Ser Leu Trp Val Met Thr Tyr Leu Lys Cys Gly Gln Lys
290 295 300

His
305

<210> 146
<211> 2567
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R21 (mGR21)

<400> 146
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tcaagtatgt tcagaaaacaa agctacatat tggggagt atataaaata tgaaggcatg 120
ccattcccaag gcatccaagg atccctgtgt attaaaaggc aacaaagcag aaccaaatgt 180
tctgtttgg acatgagctt cttccaattc aactgctgaa aaatttggat aactacatat 240
aaaactaaga acacagagtg tcacagagca gtctctgctc tccaattcac caggattaat 300
attgacagac caaaagatg tcatttaggt aaatttggta tgaatcatat tgggtcacc 360
tttggctct agaacataag ctgatagaat caaattttct ttagcagaga caatgcaa 420
tgatataaca gtgaaagaga atatatctt attgcatgt tagcaaatac cagctggatg 480
caattcatga tttctgcaa tctagtttagt tctttagaa gatataata tatataata 540
tatataata tatataata tatataata tataaacctt agtcttggaa gatatacgaa 600
agaaggattt cacaagaatg tacagagcca ttagcaaaat ttaatatac tcatcgacat 660
taggtcagtc actacataag aaggacttga atgaaagctt atcttagttt ttgagactac 720
agggacattt cacccgtcc aatgagaagc agtggatctt ctttgcggg acatggaaag 780
caatgtgtat ggtatcttaa ctatggttt gattgcagag tttgtatggaa gaaatatgag 840
caatggattt atagtgcgtaa taaactgcatt tgattgggtc aggaaaggaa ctcttttttc 900
cattgggttgg atcctgctt tcttggccat ttcaagaatg gtgttgcata gggaaatgtt 960
aataacatgg ataaaatata tgaagtattt atttcatgtt gtgactggaa cagaattac 1020
gggtatcatg tttacctggg taatttccaa tcacttcgtt ctctggctt ccactattct 1080
cagcatctt tatttgcata aaatagccag ttcttccaaa ccggttttc tctatttgc 1140
gtggagagag aagaaagtgc ttctgttgc cttctggaa aatttgcata tcttgcata 1200
caacatatta caaataaaaca aacatataca acactggatg tatcaatatg agagaaatata 1260
aacttggagt tctagagtga gtgactttgc aggttttca aatctgtct tatttggat 1320
gattgtgttgc tctgttgcata cattcacatg ggccttggc tccttcatacc tttttgcata 1380
ctccttgcgtt aaacatctac agaaaatgc tctcaatttct agagggaaac gagaccccag 1440
caactaaagcc catgtgaatg ctttgcata ttttttttgc ttccttccatcc tctatgccac 1500
ttacttcata tcttttttgc ttttttttgc tccatggca cataaaacac gactgggtct 1560
tatgttttagc ataactgttgc ggcttttca cccttcaagc cactcatca tcttgcata 1620
gggacattt aatttgcata aagccatgtt ttgggtgcata acatatttca aatgtgggca 1680
aaagcattt aatttgcata ttccatggca cggccaaacc acgtgcactt aggtatata 1740
tactactcg tggtaaagcc ctggcaac attaaccctt gaaaatata aattttgtga 1800
ctcttcgtt tttgttgcata cactcacata ttttttttgc ttttttttgc ttttttttgc 1860
gtacatgttgc gtaacaatttca aatttttata atatgttca ggcgtatca cataccctg 1920
ataactgaaa agtaagttagg atgctacata tatatttgcata tctagactt ggggcaaaaga 1980
gagacccagc tgatagctgt gcaataaaga ttttttttgc ttttttttgc ttttttttgc 2040
gaaatctatg tcactgttgc cataagcaag attttgcata actgaaacaa tcttgcata 2100
tttcttgcata ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc 2160
ttacaaaagc taaacacatg tggtttatttgcata aattttttgcata gtttttttgc ttttttttgc 2220
ggcttagtta agtgttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc 2280
taaaaaacctg gcataaaatgcata ccaatgttca aattttttgcata aatgttca cagtgcata 2340
agtaccaaga caacaaaatgcata ttttttttgcata aacccatca ttttttttgc ttttttttgc 2400
ggtatgttgcata ttactatttgcata aataagattt ttttttttgc ttttttttgc ttttttttgc 2460
aacataggaa ggcaacaatgcata ttttttttgc ttttttttgc ttttttttgc ttttttttgc 2520
agaggccact gctgactaca gcagatcatt tacaggttca gcactag 2567

<210> 147
<211> 309
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R22 (mGR22)

<400> 147

Met Ser Ser Leu Leu Glu Ile Phe Phe Val Ile Ile Ser Val Val Glu
1 5 10 15

Phe Ile Ile Gly Thr Leu Gly Asn Gly Phe Ile Val Leu Ile Asn Ser
20 25 30

Thr Ser Trp Phe Lys Asn Gln Lys Ile Ser Val Ile Asp Phe Ile Leu
35 40 45

Thr Trp Leu Ala Ile Ser Arg Met Cys Val Leu Trp Thr Thr Ile Ala
50 55 60

Gly Ala Ser Leu Arg Lys Phe Tyr Lys Thr Leu Ser Tyr Ser Lys Asn
65 70 75 80

Phe Lys Phe Cys Phe Asp Ile Ile Trp Thr Gly Ser Asn Tyr Leu Cys
85 90 95

Ile Ala Cys Thr Thr Cys Ile Ser Val Phe Tyr Leu Phe Lys Ile Ala
100 105 110

Asn Phe Ser Asn Ser Ile Phe Phe Trp Ile Lys Gln Arg Ile His Ala
115 120 125

Val Leu Leu Ala Ile Val Leu Gly Thr Leu Met Tyr Phe Ile Leu Phe
130 135 140

Leu Ile Phe Met Lys Met Ile Ala Asn Asn Phe Ile Tyr Lys Trp Thr
145 150 155 160

Lys Leu Glu Gln Asn Thr Thr Phe Pro Val Leu Asp Thr Leu Ser Gly
165 170 175

Phe Leu Val Tyr His Ser Leu Tyr Asn Gly Ile Leu Ile Phe Phe Phe
180 185 190

Ile Val Ser Leu Thr Ser Phe Leu Leu Ile Phe Ser Leu Trp Ser
195 200 205

His Leu Arg Arg Met Lys Leu Gln Gly Ile His Thr Lys Asp Ile Ser
210 215 220

Thr Glu Ala His Ile Lys Ala Met Lys Thr Met Met Ser Phe Leu Leu
225 230 235 240

Phe Phe Ile Ile Tyr Tyr Ile Ser Asn Ile Met Leu Ile Val Ala Ser
245 250 255

Ser Ile Leu Asp Asn Val Val Ala Gln Ile Phe Ser Tyr Asn Leu Ile
260 265 270

Phe Leu Tyr Leu Ser Val His Pro Phe Leu Leu Val Leu Trp Asn Ser
275 280 285

Lys Leu Lys Trp Thr Phe Gln His Val Leu Arg Lys Leu Val Cys His
290 295 300

Cys Gly Gly Tyr Ser
305

<210> 148
<211> 1488
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R22 (mGR22)

<400> 148
aaatgaataa tttcatgcaa aggataccat tagaatatga tcactattta aatttttagca 60
aatacatatt caaataccag cacaatgttt caaatttaaa atataaacat tataaaaccc 120
agcagagaac aaaatgatag ccttgataat tgggtttg ctcaagaaaa atgggtgtat 180
actttaacat ttaattggga actcagttga ggcatacat ttagggttt acagaggtat 240
tcattgccc ttaagattt ggattcacac atctacatca atgtggctgt aatccattt 300
cccatgatga aataaggtag agactgccta taaacgaca tgcgagcct actggagatt 360
ttcttgcgt tcatttcgt ttagaattc ataataggaa ctttggaaa tggatttatt 420
gtcctgataa acagtaacttc ttggcaag aatcagaaaa tctctgtaat tgatttcatt 480
cttacttggt tggccatctc cagaatgtgt gttctatgga caacaattgc tgggcctct 540
ctcaggaaat tctacaagac gttaaagtac tctaagaatt tcaaattttt ttttgacatt 600
atctggacag gatccaacta tttatgcata gcctgtacaa cgtgcacatcg tgccttctac 660
ttgttcaaga ttgccaactt ttctaatcc attttcttct ggattaaaca gagaattcat 720
gcagtaacttc tggctattgt cctaggcaca ctcatgtatt tcatttttatt tctcattttt 780
atgaaaatga tagctaataa ttttatctac aaatggacaa aattggaaaca aaacacaaca 840
ttccctgttt tagatactct aagtggttc ttagtctacc atagcctcta caatgggatt 900
ctcattttct tttttagt gtctctgacc tcatttcattt ttttaatctt ctctttatgg 960
agccaccta ggaggatgaa actacaggc atacatacca aagacataag cacagaagca 1020
cacataaaag ctatgaaaac tatgatgtca tccctttgt tcttcatcat atattatatt 1080
agcaacatta tgcttattgt ggcaagctcc attcttgaca atgtgggtgc acaaatttc 1140
tcttataacc taatatttct gtatttatct gttcatcctt ttcttcgtt tttatggac 1200
agcaaattga aatggacatt ccagcatgtt ttgagaaagc tgggtgtgtca ttgtggaggt 1260
tattcttgat ttcatgtttaat acactcaata taactgtatgg atttctaagg taagaaaaat 1320
ggaacaagga ataaagagga gaaatataatt cctttcaga tcatctgctc tgcattctg 1380
tccttagcat gctattaaga attgttgact aaatccagtc atttttaaca tgaggaaagg 1440
atgtttcaat ccaacttaga gagggtacaa aatagtcata ggaggcag 1488

<210> 149
<211> 333
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R23 (mGR23)

<400> 149
Met Phe Ser Gln Lys Ile Asn Tyr Ser His Leu Phe Thr Phe Ser Ile
1 5 10 15
Thr Leu Tyr Val Glu Ile Val Thr Gly Ile Leu Gly His Gly Phe Ile
20 25 30
Ala Leu Val Asn Ile Met Asp Trp Val Lys Arg Arg Arg Ile Ser Ser
35 40 45
Val Asp Gln Ile Leu Thr Ala Leu Ala Leu Thr Arg Phe Ile Tyr Val
50 55 60
Leu Ser Met Leu Ile Cys Ile Leu Leu Phe Met Leu Cys Pro His Leu
65 70 75 80

<210> 150
<211> 1442
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R23 (mGR23)

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<400> 150
aattttcagc aacccaatatg tagactgctt aaatgcataa gaaacattat aaattgaagc 60
atgtttcac agaaaataaa ctacagccat ttgtttactt tttcaatcac cttgtatgtg 120
gaaataqtaa cqqaatctt aqqacatqqa ttcataqcat tagtgaacat catggactgg 180
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gtcaaaagaa gaaggatctc ttcaagtggat cagattctca ctgcttggc ccttaccaga 240
 ttcatttatg tcttgcstat gctgatttgc atattgttat tcattgtgtg cccacattt 300
 cctaggagat cagaatgc ttcagcaatg ggtattttct gggtagtcaa cagccattt 360
 agcatctggc ttactacatg ctcgggtgc ttttattttc tcaagatagc caattttct 420
 aactctttt ttcttatct aaagtggaga gttaaaaaaag tgattttaat aataatcctg 480
 gcatcaactga ttttcttgac ttacacatt ttatcttag ggatataatga tcagttctca 540
 attgctgctt atgttaggaaa tatgtcttat agttgacag atttaacaca atttccagt 600
 actttcttat tctccaactc atccaatgtt ttcttaatca ccaactcatc ccatgtttc 660
 ttacccatca actccctgtt catgctcata cccttcacag tgccttggt agccttctc 720
 atgctcatct tctcaactgtg gaagcatcac aaaaagatgc aggtcaatgc caaacaacct 780
 agagatgtca gtactatggc ccacattaaa gccttgcata ctgtgtctc cttcctgctg 840
 ctgtatgcca tatacttact tttccttatac ataggaattt tgaaccttgg attgatggag 900
 aaaatagtga tactgatatt tgaccacatt tctggagcag ttttcctat aagccactca 960
 tttgtactga ttctggaaa cagtaagctg agacaagcca gtcttctgt gtgccttg 1020
 ctaagggtgcc agtccaaaga tatggacacc atgggtctct agtaaattcc agagtacatt 1080
 ttgtaaaaat cttgaggatg atcagttcat agaaaaaaatg taccttatgg gggaaaataa 1140
 aaagtggggc ttcaatcctg ggagtaataa tacacaggag ggtaggacag catgaaggag 1200
 actagacta tataagtggc ctcatacagg atatggaaa ggaaagattt atgcaataaa 1260
 gagggagatc atattggagg atgaggagc attacatatg taaaatgact ataagaatgg 1320
 aatcatgcta atctaaaaaa atctgtaatg catttcattc agactatata catatatgcc 1380
 tatatatgga tataatgggaa tatatatatttct atacatattt taaaagaacc tttcttataat 1440
 ag

<210> 151
 <211> 309
 <212> PRT
 <213> Mus sp.

<220>
 <223> mouse T2R24 (mGR24)

<400> 151
 Met Val Pro Val Leu His Ser Leu Ser Thr Ile Ile Leu Ile Ala Glu
 1 5 10 15
 Phe Val Trp Gly Asn Leu Ser Asn Gly Leu Ile Val Leu Lys Asn Cys
 20 25 30
 Ile Asp Trp Ile Asn Lys Lys Glu Leu Ser Thr Val Asp Gln Ile Leu
 35 40 45
 Ile Val Leu Ala Ile Ser Arg Ile Ser Leu Ile Trp Glu Thr Leu Ile
 50 55 60
 Ile Trp Val Lys Asp Gln Leu Ile Ser Ser Ile Thr Ile Glu Glu Leu
 65 70 75 80
 Lys Ile Ile Val Phe Ser Phe Ile Leu Ser Ser His Phe Ser Leu Trp
 85 90 95
 Leu Ala Thr Ala Leu Ser Ile Phe Tyr Leu Phe Arg Ile Pro Asn Cys
 100 105 110
 Tyr Trp Gln Ile Phe Leu Tyr Leu Lys Trp Arg Ile Lys Gln Leu Ile
 115 120 125
 Val His Met Leu Leu Gly Ser Leu Val Phe Leu Val Ala Asn Met Ile
 130 135 140

Gln Ile Thr Ile Thr Leu Glu Glu Arg Phe Tyr Gln Tyr Gly Gly Asn
 145 150 155 160
 Thr Ser Val Asn Ser Met Glu Thr Glu Phe Ser Ile Leu Ile Glu Leu
 165 170 175
 Met Leu Phe Asn Met Thr Met Phe Ser Ile Ile Pro Phe Ser Leu Ala
 180 185 190
 Leu Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln
 195 200 205
 Lys Met Pro Leu Asn Ser Arg Gly Asp Arg Asp Pro Ser Ala Thr Ala
 210 215 220
 His Arg Asn Ala Leu Arg Ile Leu Val Ser Phe Leu Leu Leu Tyr Thr
 225 230 235 240
 Ile Tyr Phe Leu Ser Leu Leu Ile Ser Trp Val Ala Gln Lys Asn Gln
 245 250 255
 Ser Glu Leu Val His Ile Ile Cys Met Ile Thr Ser Leu Val Tyr Pro
 260 265 270
 Ser Phe His Ser Tyr Ile Leu Ile Leu Gly Asn Tyr Lys Leu Lys Gln
 275 280 285
 Thr Ser Leu Trp Val Met Arg Gln Leu Gly Cys Arg Met Lys Arg Gln
 290 295 300
 Asn Thr Pro Thr Thr
 305

<210> 152
 <211> 1465
 <212> DNA
 <213> Mus sp.

<220>
 <223> mouse T2R24 (mGR24)

<400> 152
 caaagaggag aaatatttag ctacacagtg taccacatac aagccgttca atcagtataa 60
 ggggagcagt catatagaat ttgggcttc tttcttttaa tatggcacct gttctgcaca 120
 gtctctccac catcatacta attgcagagt ttgtttgggg aaatttgagc aatgggttga 180
 tagtgttcaa gaactgcatt gactggatca ataaaaaaga gctctccaca gttgatcaaa 240
 tactcattgt cttggcaatt tcaagaatta gtctcatctg ggaaacacta attatatggg 300
 ttaaagatca actaattca tctattacta ttgaagaatt aaaaataatt gtgttcagct 360
 ttatactatc tagccacttc agtctctggc ttgctacagc tctcagcatc ttctatttat 420
 tcagaatacc taattgctac tggcagatct ttctctactt gaaatggaga ataaagcaac 480
 tgattgtcca catgcttctg ggaagctgg tggcttgggt tgcaaatatg atacagataa 540
 ccatcactct tgaagagagg ttctatcaat atggaggaaa tacaagtgtt aattccatgg 600
 agactgagtt ctcaattttt atagagctga tggattttaa catgactatg ttctccattt 660
 taccattttc attggcctta atttctttc ttctgctaat cttctcttta tggaaacatc 720
 tccagaagat gccactcaat tcttagaggag atagagaccc tagtgcacg gcccacagaa 780
 atgccttggag aattttggtc tccttcctct tgctctatac tatatatttc ctgtctcttc 840
 ttatatcatg ggttgctcag aagaatcaa gtgaactggt tcacattatt tggatgataa 900
 cttcactcgt gtatccctca ttccactcat atatcctgat tctgggaaat tataaattaa 960
 agcagacctc tcttgggtt atgaggcagc tggatgttag gatgaaaaga cagaatacac 1020
 caactacata aggcagccaa acagtctatt gggttttaga taacaaatct aaatctatga 1080

ggaagtagtt caataacatt tttccccttg acatggagta gcagggtttt tttttattag 1140
atattttctt tacttacatt tcaaatgcta tcccgaaaat tccctgtacc ctctccctgt 1200
cctgttcccc tacccaccca ctcccacttc ttggccctgg cattccctg gagtatacg 1260
tttttattag tcaaactatc tcactgacta aggtcataa aacaagttat tttaacacta 1320
atttcaatta aatcaaaggt aaagtgtcag cacatgcctt taatcacaca attccatcaa 1380
attcagcact caggagaggg tgatctctgt gaattccagc acactggcgg ccgttactag 1440
tggatccgag ctccgtacca agtt 1465

<210> 153
<211> 311
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R25 (mGR25)

<400> 153
Met Met Gly Ile Ala Ile Asp Ile Leu Trp Ala Ala Ile Ile Ile Val
1 5 10 15

Gln Phe Ile Ile Gly Asn Ile Ala Asn Gly Phe Ile Ala Leu Val Asn
20 25 30

Ile Ile Asp Trp Val Lys Arg Arg Lys Ile Ser Leu Met Asp Lys Ile
35 40 45

Ile Thr Ala Leu Ala Ile Ser Arg Ile Tyr Leu Leu Trp Ser Thr Phe
50 55 60

Leu Ile Thr Leu Thr Ser Ser Leu Asp Pro Asp Ile Lys Met Ala Val
65 70 75 80

Lys Ile Ile Arg Ile Ser Asn Asn Thr Trp Ile Ile Ala Asn His Phe
85 90 95

Ser Ile Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe Leu Lys Ile
100 105 110

Ala Asn Phe Ser Asn Tyr Ile Phe Leu Tyr Leu Arg Trp Arg Phe Lys
115 120 125

Lys Val Val Ser Val Thr Leu Leu Ile Ser Leu Ile Phe Leu Leu Leu
130 135 140

Asn Ile Leu Leu Met Asn Met His Ile Asp Ile Trp Ser Asp Lys Ser
145 150 155 160

Lys Arg Asn Leu Ser Phe Ser Val Arg Ser Asn Asn Cys Thr Gln Phe
165 170 175

Pro Arg Leu Val Leu Leu Ile Asn Thr Met Phe Thr Ser Ile Pro Phe
180 185 190

Thr Val Ser Leu Leu Ala Phe Leu Leu Ile Phe Ser Leu Trp Arg
195 200 205

His Leu Lys Thr Met Gln Tyr Tyr Ala Lys Gly Ser Glu Asp Thr Thr
210 215 220

Thr Ala Ala His Ile Lys Ala Leu His Met Val Val Ala Phe Leu Leu
225 230 235 240

Phe Tyr Thr Val Phe Phe Leu Ser Leu Ala Ile Gln Tyr Trp Thr Ser
245 250 255

Gly Ser Gln Glu Asn Asn Asn Leu Phe Tyr Ala Thr Ile Val Ile Thr
260 265 270

Phe Pro Ser Val His Ser Cys Ile Leu Ile Leu Arg Asn Ser Gln Leu
275 280 285

Arg Gln Ala Ser Leu Leu Val Leu Trp Trp Leu Leu Cys Lys Ser Lys
290 295 300

Asp Val Arg Met Leu Val Pro
305 310

<210> 154
<211> 1103
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R25 (mGR25)

<400> 154
aaaactattc gaattgaaca cagtaaccaa ttcttcagcg gacttacaca aatcaagcta 60
ttatcttatg gatgatgggt attgccatag atatcttatg ggcagctatt atcattgtgc 120
aattcataat tggaaatatt gcaaatggat tcatacgattt ggtgaacatc atagactggg 180
tgaagagaag aaaaatctct ttaatggata agatcattttc tgcttggca atctcttagga 240
tttatctgtc gtggcttaca ttcttaatata cactaacatc ttcactggat ccagatattta 300
aaatggctgt gaaaatcattt agaataagca ataacacctg gattattgca aatcatttca 360
gcattttgggt tgctacatgt ctcagcatct tttatatttctt caagatagcc aatttttctt 420
actatatttt tctctactta aggtggagat ttaagaaggt ggttttagt acattgctaa 480
tctctttat cttcctgtt ttaaatattt tactgtatgaa catgcattt gatatctgg 540
gtgataagtc caaaagaaac ctttctttt gtgtcagatc aaataattgc actcagtttc 600
ccagacttgt ccttttaatc aacacaatgt tcacatcaat ccccttcaact gtgtccctgt 660
tggcttttctt gcttctcatc ttctccctgt ggagacacctt gaaaaccatg caataactatg 720
ctaaaggctc cgaagacacc accacagctg cacatataaa ggccttgcac atggtagtgg 780
cctttctctt gttctacaca gttttctttt tgctcttgc catacaatat tgacaccttg 840
ggtctcaaga gaataacaac ctgtttttagt ccacaattgt aattacttcc ctttcgtcc 900
attcatgtat cctgattctg agaaacagcc agctgaggca ggcacatctg ttggtgctgt 960
ggtggctgtc gtgcaagtcc aaagatgtac ggatgttggt tccctgaaat actctgtcaa 1020
tgctcttttag tagtgaagaa gaaaatagct tagttaagga aattctgtt cattaccgaa 1080
gtataactttc aagtttatgt atc 1103

<210> 155
<211> 308
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R26 (mGR26)

<400> 155
Met Leu Pro Thr Leu Ser Val Phe Phe Met Leu Thr Phe Val Leu Leu
1 5 10 15

Cys Phe Leu Gly Ile Leu Ala Asn Gly Phe Ile Val Leu Met Leu Ser
 20 25 30

Arg Glu Trp Leu Leu Arg Gly Arg Leu Leu Pro Ser Asp Met Ile Leu
 35 40 45

Phe Ser Leu Gly Thr Ser Arg Phe Phe Gln Gln Cys Val Gly Leu Val
 50 55 60

Asn Ser Phe Tyr Tyr Phe Leu His Leu Val Glu Tyr Ser Gly Ser Leu
 65 70 75 80

Ala Arg Gln Leu Ile Ser Leu His Trp Asp Phe Leu Asn Ser Ala Thr
 85 90 95

Phe Trp Phe Cys Thr Trp Leu Ser Val Leu Phe Cys Ile Lys Ile Ala
 100 105 110

Asn Phe Ser His Pro Ala Phe Leu Trp Leu Lys Trp Arg Phe Pro Ala
 115 120 125

Leu Val Pro Trp Phe Leu Leu Gly Ser Ile Leu Val Ser Val Ile Val
 130 135 140

Thr Leu Leu Phe Phe Trp Gly Asn His Thr Ile Tyr Gln Ala Phe Leu
 145 150 155 160

Arg Arg Lys Phe Thr Gly Asn Thr Thr Phe Lys Glu Trp Asn Arg Arg
 165 170 175

Leu Glu Ile Asp Tyr Phe Met Pro Leu Lys Val Val Thr Met Ser Ile
 180 185 190

Pro Cys Ser Leu Phe Leu Val Ser Ile Leu Leu Ile Ser Ser Leu
 195 200 205

Arg Arg His Ser Leu Arg Met Gln His Asn Thr His Ser Leu Gln Asp
 210 215 220

Pro Asn Val Gln Ala His Ser Arg Ala Leu Lys Ser Leu Ile Ser Phe
 225 230 235 240

Leu Val Leu Tyr Ala Val Ser Phe Val Ser Met Ile Ile Asp Ala Thr
 245 250 255

Val Phe Ile Ser Ser Asp Asn Val Trp Tyr Trp Pro Trp Gln Ile Ile
 260 265 270

Leu Tyr Phe Cys Met Ser Val His Pro Phe Ile Leu Ile Thr Asn Asn
 275 280 285

Leu Arg Phe Arg Gly Thr Phe Arg Gln Leu Leu Leu Leu Ala Arg Gly
 290 295 300

Phe Trp Val Ala
 305

<210> 156
<211> 3437
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R26 (mGR26)

agaaaaaagac ttaagaatct caccttaca aaaaaaaaaa aaaaagaatc tcacttattt 3180
tatattcaaa ttccattttt aaaaagaaaa gcacagcatt aattttcta aatactgtt 3240
ataaaaataa cttgctctaa gaattataca aatgtttga aaggtaactt tgaaaaaaa 3300
gtgtgattag acatggatgt ttgtaagaca gaacaaagag ctcttggaaag tccatggcag 3360
ctcattggtc ttgccttcag tagagcctgt ctgaatcctg taacctctta tgccctttt 3420
tagctttct gcagatc 3437

<210> 157
<211> 340
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R27 (mGR27)

<400> 157
gaattcggcc ttgcgggatc cgggaacgga ttcatagcac tggtaaactt catgggctgg 60
atgaagaata ggaagattgc ctccatttgat ttaatcctca caagtctggc catatccaga 120
atttgtctat tgcgtatc actatttagat tggtttatat tggtgcata tccagatgtc 180
tatgccactg gtaaagaaat gagaatcatt gacttcttct ggacactaac caatcactta 240
agtatcttgtt ttgcaacctg cctcagcatt tactatttct tcaagatagg taatttcttt 300
caccactt tcctatgcct caagtctaga cgccaaggc 340

<210> 158
<211> 82
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R28 (mGR28)

<400> 158
Gly Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile
1 5 10 15
Leu Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr
20 25 30
Val His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly
35 40 45
Leu Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala
50 55 60
Thr Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile
65 70 75 80
Ala Asn

<210> 159
<211> 341
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R28 (mGR28)

<400> 159
gaattcgccc ttgcgggatc cgggaacggg tttattgtgc tggtgctggg cagggagtgg 60
ctgcgatatg gcagggttgct gcccggat atgatcctca ttagcttggg tgcctccgc 120
ttctgcctgc agttgggtgg gacggtgac aacttctact actctgccc aaggtcgag 180
tactctgggg gtctcggccg acagttcttc catctacact ggcacttcct gaactcagcc 240
accttctggt ttgcagctg gctcagtgct ctgttctgtg tgaagattgc taacatcaca 300
cactccacct tcctgtgtct caagtctaga cgccaaggc g 341

<210> 160
<211> 320
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R29 (mGR29)

<400> 160
Met Asp Gly Ile Val Gln Asn Met Phe Thr Phe Ile Val Ile Val Glu
1 5 10 15
Ile Ile Ile Gly Trp Ile Gly Asn Gly Phe Ile Ala Leu Val Asn Cys
20 25 30
Ile His Trp Tyr Lys Arg Arg Lys Ile Ser Ala Leu Asn Gln Ile Leu
35 40 45
Thr Ala Leu Ala Phe Ser Arg Ile Tyr Leu Leu Leu Thr Val Phe Thr
50 55 60
Val Ile Ala Val Ser Thr Leu Tyr Thr His Val Leu Val Thr Arg Arg
65 70 75 80
Val Val Lys Leu Ile Asn Phe His Leu Leu Phe Ser Asn His Phe Ser
85 90 95
Met Trp Leu Ala Ala Cys Leu Gly Leu Tyr Tyr Phe Leu Lys Ile Ala
100 105 110
His Phe Pro Asn Ser Ile Phe Val Tyr Leu Lys Met Arg Ile Asn Gln
115 120 125
Val Val Ser Gly Thr Leu Leu Met Ser Leu Gly Leu Leu Phe Leu Asn
130 135 140
Thr Leu Leu Ile Asn Ser Tyr Ile Asp Thr Lys Ile Asp Asp Tyr Arg
145 150 155 160
Glu His Leu Leu Tyr Asp Phe Thr Ser Asn Asn Thr Ala Ser Phe Tyr
165 170 175
Arg Val Ile Leu Val Ile Asn Asn Cys Ile Phe Thr Ser Ile Pro Phe
180 185 190
Thr Leu Ser Gln Ser Thr Phe Leu Leu Leu Ile Phe Ser Leu Trp Arg
195 200 205
His Tyr Lys Lys Met Gln Gln His Ala Gln Arg Cys Arg Asp Val Leu
210 215 220

Ala Asp Ala His Ile Arg Val Leu Gln Thr Met Val Thr Tyr Val Leu
225 230 235 240

Leu Cys Ala Ile Phe Phe Leu Ser Leu Ser Met Gln Ile Leu Arg Ser
245 250 255

Glu Leu Leu Lys Asn Ile Leu Tyr Val Arg Phe Cys Glu Ile Val Ala
260 265 270

Ala Val Phe Pro Ser Gly His Ser Cys Val Leu Ile Cys Arg Asp Thr
275 280 285

Asn Leu Arg Gly Thr Phe Leu Ser Val Leu Ser Trp Leu Lys Gln Arg
290 295 300

Phe Thr Ser Trp Ile Pro Asn Ile Asn Cys Arg Ser Ser Cys Ile Phe
305 310 315 320

<210> 161
<211> 1108
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R29 (mGR29)

<400> 161
agcttgcata ttactgcaca gagtttttt taaaaattga gtttgttag 60
tggattcaat actcagatag agctcttaa ttttttaca gtgacccat gaatcataac 120
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aaataataat aggatggatt ggaaatggat tcatactct ggtgaactgc atacactgg 240
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tagatgacta cagagaacat ctactgtatg atttcacttc gaataatact gcttcatttt 660
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agtccacttt tctcctgctc atcttctccc tggagaca ttacaagaag atgcaacagc 780
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<210> 162
<211> 312
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R30 (mGR30)

<400> 162
Met Thr Tyr Glu Thr Asp Thr Thr Leu Met Leu Val Ala Val Gly Glu
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Ala Leu Val Gly Ile Leu Gly Asn Ala Phe Ile Ala Leu Val Asn Phe
 20 25 30

Met Gly Trp Met Lys Asn Arg Lys Ile Ala Ser Ile Asp Leu Ile Leu
 35 40 45

Ser Ser Val Ala Met Ser Arg Ile Cys Leu Gln Cys Ile Ile Leu Leu
 50 55 60

Asp Cys Ile Ile Leu Val Gln Tyr Pro Asp Thr Tyr Asn Arg Gly Lys
 65 70 75 80

Glu Met Arg Thr Val Asp Phe Phe Trp Thr Leu Thr Asn His Leu Ser
 85 90 95

Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Leu Phe Lys Ile Ala
 100 105 110

Asn Phe Phe His Pro Leu Phe Leu Trp Ile Lys Trp Arg Ile Asp Lys
 115 120 125

Leu Ile Leu Arg Thr Leu Leu Ala Cys Val Ile Ile Ser Leu Cys Phe
 130 135 140

Ser Leu Pro Val Thr Glu Asn Leu Ser Asp Asp Phe Arg Arg Cys Val
 145 150 155 160

Lys Thr Lys Glu Arg Ile Asn Ser Thr Leu Arg Cys Lys Val Asn Lys
 165 170 175

Ala Gly His Ala Ser Val Lys Val Asn Leu Asn Leu Val Met Leu Phe
 180 185 190

Pro Phe Ser Val Ser Leu Val Ser Phe Leu Leu Leu Ile Leu Ser Leu
 195 200 205

Trp Arg His Thr Arg Gln Ile Gln Leu Ser Val Thr Gly Tyr Lys Asp
 210 215 220

Pro Ser Thr Thr Ala His Val Lys Ala Met Lys Ala Val Ile Ser Phe
 225 230 235 240

Leu Ala Leu Phe Val Val Tyr Cys Leu Ala Phe Leu Ile Ala Thr Ser
 245 250 255

Ser Tyr Phe Met Pro Glu Ser Glu Leu Ala Val Ile Trp Gly Glu Leu
 260 265 270

Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly
 275 280 285

Ser Ser Lys Leu Lys Gln Ala Ser Val Arg Val Leu Cys Arg Val Lys
 290 295 300

Thr Met Leu Lys Gly Lys Lys Tyr
 305 310

<210> 163
<211> 3775
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R30 (mGR30)

<400> 163
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caaatagtag ctcagcctaa attaactgtg tgtagaaaaa aatgacctgc ggagaagata 240
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gatttagata aactatctac agtcttcatt tataattctc atcttcattca caagacagac 360
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aactgcatca aatcagccag aaactaattt gatacttctc tacattaaaa tgacatacga 480
aacagatact accttaatgc ttgttagctgt tggtgaggcc ttagtaggga ttttaggaaa 540
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tgatttaatc ctctcaagtg tggccatgtc cagaatttgc ctacagtgtt taatccatt 660
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cggtgacttc ttctggacac ttaccaacca ttaagtgtc tggggccca cctgcctcag 780
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<210> 164
<211> 310
<212> PRT
<213> Mus sp.

<220>
<223> mouse T2R31 (mGR31)

<400> 164
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Asn Met Phe Ile Gly Leu Ala Asn Cys Ser Asp Trp Val Lys Asn Gln
20 25 30
Lys Ile Thr Phe Ile Asn Phe Ile Met Val Cys Leu Ala Ala Ser Arg
35 40 45
Ile Ser Ser Val Leu Met Leu Phe Ile Asp Ala Thr Ile Gln Glu Leu
50 55 60
Ala Pro His Phe Tyr Tyr Ser Tyr Arg Leu Val Lys Cys Ser Asp Ile
65 70 75 80
Phe Trp Val Ile Thr Asp Gln Leu Ser Thr Trp Leu Ala Thr Cys Leu
85 90 95
Ser Ile Phe Tyr Leu Phe Lys Val Ala His Ile Ser His Pro Leu Phe
100 105 110
Leu Trp Leu Lys Trp Arg Leu Arg Gly Val Leu Val Val Phe Leu Val
115 120 125
Phe Ser Leu Phe Leu Leu Ile Ser Tyr Phe Leu Leu Glu Thr Leu
130 135 140
Pro Ile Trp Gly Asp Ile Tyr Val Thr Leu Lys Asn Asn Leu Thr Leu
145 150 155 160
Phe Ser Gly Thr Ile Lys Thr Thr Ala Phe Gln Lys Ile Ile Val Phe
165 170 175
Asp Ile Ile Tyr Leu Val Pro Phe Leu Val Ser Leu Ala Ser Leu Leu
180 185 190
Leu Leu Phe Leu Ser Leu Val Lys His Ser Arg Ser Leu Asp Leu Ile
195 200 205

Ser Thr Thr Ser Glu Asp Ser Arg Thr Lys Ile His Lys Lys Ala Met
210 215 220

Lys Met Leu Val Ser Phe Leu Ile Leu Phe Ile Ile His Ile Phe Phe
225 230 235 240

Met Gln Leu Ala Arg Trp Leu Leu Phe Leu Phe Pro Met Ser Arg Pro
245 250 255

Ile Asn Phe Ile Leu Thr Leu Asn Ile Phe Ala Leu Thr His Ser Phe
260 265 270

Ile Leu Ile Leu Gly Asn Ser Asn Leu Arg Gln Arg Ala Met Arg Ile
275 280 285

Leu Gln His Leu Lys Ser Gln Leu Gln Glu Leu Ile Leu Ser Leu His
290 295 300

Arg Phe Ser Ser Leu Tyr
305 310

<210> 165
<211> 4675
<212> DNA
<213> Mus sp.

<220>
<223> mouse T2R31 (mGR31)

<220>
<221> modified_base
<222> (1)..(4675)
<223> n = g, a, c or t

<400> 165
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agagattaga cagaaaaata agtttctaa caactgtttt agatagggtc atgaaatgac 180
ataaaaacacc aatgctaagg caatccatta tgttttctca tgaggagccc atatgtacac 240
ttgagtgtgt cttattattt ccctgagtgta tttttaattt ttattaaaca cttaactgtg 300
attcatacta gttagttctg aaattctttt cttcatcaaa gccattaatc ctgggggttt 360
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4675

<210> 166
<211> 20
<212> PRT
<213> Artificial Sequence

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<220>
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      consensus sequence 1, T2R transmembrane region 1

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<222> (2)
<223> Xaa = Phe or Ala

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Ile, Val or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Val or Leu

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Leu or Val

<220>
<221> MOD_RES
<222> (10)
<223> Xaa = Gly or Thr

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Val or Ala

<220>
<221> MOD_RES
<222> (18)
<223> Xaa = Ile or Met

<400> 166
Glu Xaa Xaa Xaa Gly Xaa Xaa Gly Asn Xaa Phe Ile Xaa Leu Val Asn
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Cys Xaa Asp Trp
    20

<210> 167
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
      consensus sequence 2, T2R transmembrane region 2

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<220>
<221> MOD_RES
<222> (1)
<223> Xaa = Asp or Gly

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Phe or Leu

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Ile or Leu

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Thr or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Gly, Ala or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Cys, Gly or Phe

<400> 167
Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu
    1           5           10

<210> 168
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
      consensus sequence 3, T2R transmembrane region 3

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Leu or Phe

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Ser, Thr or Asn

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Leu, Ile or Val

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<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Phe or Leu

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = Ala or Thr

<220>
<221> MOD_RES
<222> (10)
<223> Xaa = Cys, Ser or Asn

<220>
<221> MOD_RES
<222> (12)
<223> Xaa = Ser, Asn or Gly

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Ile or Val

<400> 168
Asn His Xaa Xaa Xaa Trp Xaa Xaa Thr Xaa Leu Xaa Xaa
1 5 10

<210> 169
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
consensus sequence 4, T2R transmembrane region 4

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Phe or Cys

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = Asn or Ser

<220>
<221> MOD_RES
<222> (11)
<223> Xaa = His or Asn

<220>
<221> MOD_RES
<222> (12)
<223> Xaa = Pro or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Leu, Ile or Val

<220>
<221> MOD_RES
<222> (16)
<223> Xaa = Trp or Tyr

<400> 169
Phe Tyr Xaa Leu Lys Ile Ala Xaa Phe Ser Xaa Xaa Xaa Phe Leu Xaa
1 5 10 15

Leu Lys

<210> 170
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
consensus sequence 5, T2R transmembrane region 5

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Ile, Phe or Val

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = Lys or Arg

<220>
<221> MOD_RES
<222> (10)
<223> Xaa = Ser or Thr

<220>
<221> MOD_RES
<222> (11)
<223> Xaa = Lys or Arg

<220>
<221> MOD_RES
<222> (12)
<223> Xaa = Gln or Lys

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Met or Ile

<220>
<221> MOD_RES
<222> (14)
<223> Xaa = Gln or Lys

<400> 170
Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa
1 5 10

<210> 171
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:T2R family
consensus sequence 6, T2R transmembrane region 7

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = Phe or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Leu or Met

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (10)
<223> Xaa = Pro, Ser or Asn

<220>
<221> MOD_RES
<222> (13)
<223> Xaa = Lys or Arg

<220>
<221> MOD_RES
<222> (14)
<223> Xaa = Gln or Arg

<400> 171
His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa
1 5 10

<210> 172
<211> 300
<212> PRT
<213> Mus sp.

<220>
<223> mT2R5

<220>
<221> MOD_RES
<222> (44)
<223> Xaa = Ile or Thr

<220>
<221> MOD_RES
<222> (85)
<223> Xaa = Val or Ile

<220>
<221> MOD_RES
<222> (101)
<223> Xaa = Ala or Thr

<220>
<221> MOD_RES
<222> (155)
<223> Xaa = Asp or Gly

<220>
<221> MOD_RES
<222> (294)
<223> Xaa = Arg or Leu

<400> 172
Met Leu Ser Ala Ala Glu Gly Ile Leu Leu Ser Ile Ala Thr Val Glu
1 5 10 15

Ala Gly Leu Gly Val Leu Gly Asn Thr Phe Ile Ala Leu Val Asn Cys
20 25 30

Met Asp Trp Ala Lys Asn Asn Lys Leu Ser Met Xaa Gly Phe Leu Leu
35 40 45

Ile Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Leu Leu Thr Leu
50 55 60

Asp Ala Tyr Ala Lys Leu Phe Tyr Pro Ser Lys Tyr Phe Ser Ser Ser
65 70 75 80

Leu Ile Glu Ile Xaa Ser Tyr Ile Trp Met Thr Val Asn His Leu Thr
85 90 95

Val Trp Phe Ala Xaa Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
100 105 110

Asn Phe Ser Asp Cys Val Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys
115 120 125

Ala Phe Val Phe Leu Leu Gly Cys Leu Leu Thr Ser Trp Val Ile Ser
130 135 140

Phe Ser Phe Val Val Lys Val Met Lys Asp Xaa Lys Val Asn His Arg
145 150 155 160

Asn Arg Thr Ser Glu Met Tyr Trp Glu Lys Arg Gln Phe Thr Ile Asn
165 170 175

Tyr Val Phe Leu Asn Ile Gly Val Ile Ser Leu Phe Met Met Thr Leu
180 185 190

Thr Ala Cys Phe Leu Leu Ile Met Ser Leu Trp Arg His Ser Arg Gln
195 200 205

Met Gln Ser Gly Val Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His
210 215 220

Val Lys Ala Ile Lys Phe Leu Ile Ser Phe Ile Ile Leu Phe Val Leu
225 230 235 240

Tyr Phe Ile Gly Val Ser Ile Glu Ile Ile Cys Ile Phe Ile Pro Glu
245 250 255

Asn Lys Leu Leu Phe Ile Phe Gly Phe Thr Thr Ala Ser Ile Tyr Pro
260 265 270

Cys Cys His Ser Phe Ile Leu Ile Leu Ser Asn Ser Gln Leu Lys Gln
275 280 285

Ala Phe Val Lys Val Xaa Gln Leu Leu Lys Phe Phe
290 295 300